EG014US-Sequence Listing.txt Page 1

IAP20 Rec'd FCT/FTO 27 JAN 2006

SEQUENCE LISTING

```
<110> FUJII, Kazutoshi
             IIBOSHI, Masae
YANASE, Michiyo
             TAKATA, Hiroki
            TAKAHA, Takeshi
KURIKI, Takashi
<120> A METHOD FOR IMPROVING THE THERMOSTABILITY OF SUCROSE PHOSPHORYLASE (SP)
<130> EG014US
<140>
            PCT/JP2004/012533
            2004-08-31
<150> JP2003-313305
<151> 2003-09-04
<160> 27
<170> Patentin version 3.3
<210><211><211><212>
            1443
            DNA
            Streptococcus mutans
<220>
<221> CDS
<222> (1)..(1443)
atg cca att aca aat aaa aca atg ttg att act tac gca gac agt ttg
Met Pro IIe Thr Asn Lys Thr Met Leu IIe Thr Tyr Ala Asp Ser Leu
1 5 10 15
96
gat gct gtt ggc ggt gtc cat ttg ctg cca ttc ttt cct tcc aca ggt Asp Ala Val Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly 35 40 45
                                                                                                                          144
                                                                                                                          192
gat cgt ggc ttt gca ccg att gat tac cat gaa gtt gac tct gct ttt
Asp Arg Gly Phe Ala Pro lle Asp Tyr His Glu Val Asp Ser Ala Phe
50 55 60
ggc gat tgg gat gat gtc aaa cgt ttg ggt gaa aaa tat tac ctc atg
Gly Asp Trp Asp Asp Vai Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met
65 70 75 80
                                                                                                                          240
ttt gat ttc atg att aat cat att tcg cgt cag tct aaa tat tat aaa
Phe Asp Phe Met IIe Asn His IIe Ser Arg Gln Ser Lys Tyr Tyr Lys
85 90 95
                                                                                                                          288
gat tac caa gaa aag cat gaa gca agt gct tat aaa gat cta ttt tta
Asp Tyr Gln Glu Lys His Glu Ala Ser Ala Tyr Lys Asp Leu Phe Leu
100 105 110
                                                                                                                          336
aat tgg gat aaa ttt tgg cct aaa aat cgc ccg aca caa gaa gat gtg
Asn Trp Asp Lys Phe Trp Pro Lys Asn Arg Pro Thr Gin Giu Asp Val
115 120 125
                                                                                                                          384
gac ctg att tat aag cgt aag gat cga gca cct aag cag gaa atc caa
Asp Leu lle Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gin Giu ile Gin
130 140
                                                                                                                          432
ttt gca gat ggc agt gtt gaa cat ctc tgg aac act ttt ggg gag gaa
Phe Ala Asp Gly Ser Val Glu His Leu Trp Asn Thr Phe Gly Glu Glu
145 155 160
                                                                                                                          480
cag att gat ctt gac gtg act aaa gaa gtg act atg gat ttt att cgc
Gin lie Asp Leu Asp Val Thr Lys Giu Val Thr Met Asp Phe lie Arg
165 170 175
                                                                                                                          528
tct acc att gaa aat tta gca gcc aac ggc tgt gat ctc att cgt ttg
Ser Thr lle Glu Asn Leu Ala Ala Asn Gly Cys Asp Leu lle Arg Leu
180 190
                                                                                                                         576
gat gcc ttt gct tat gct gtt aaa aag cta gat acg aat gat ttc ttt
Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe
                                                                                                                         624
```

195	20	00	205	
gtt gaa cct gaa Val Glu Pro Glu 210	atc tgg act ct lie Trp Thr Le 215	eu Leu Asp Lys	gtt ogt gat ata Val Arg Asp 11e 220	gct 672 Ala
gct gta tcg ggt Ala Val Ser Gly 225				
att caa ttt aaa lle Gin Phe Lys	att gca gac ca lle Ala Asp Hi 245	at gat tac tat is Asp Tyr Tyr 250	gtt tat gat ttt Val Tyr Asp Phe 255	Ala
ctg cct atg gtg Leu Pro Met Val 260				
ctt gcc aaa tgg Leu Ala Lys Trp 275		er Pro Met Lys		
gat aca cat gac Asp Thr His Asp 290	ggt att ggt gt Gly lie Gly Va 295	al Val Asp Val	aag gat atc ctg Lys Asp lle Leu 300	act 912 Thr
gac gaa gaa att Asp Glu Glu Ile 305				
aat gtc aat cgt Asn Val Asn Arg	aag tat tca ac Lys Tyr Ser Th 325	ct gcc gaa tat hr Ala Giu Tyr 330	aat aac ttg gat Asn Asn Leu Asp 335	
tat caa att aat Tyr Gin lie Asn 340				
aaa tac ttt ttg Lys Tyr Phe Leu 355		le Gin Ala Phe		
cag gtt tat tac Gln Val Tyr Tyr 370		eu Ala Gly Lys .		
ctg gaa agc act Leu Glu Ser Thr 385				
agt gaa gaa att Ser Glu Glu lle				Leu
tta aat ctc ttt Leu Asn Leu Phe 420	Thr Tyr Arg As	sn Gin Ser Aia 425	Ala Phe Asp Leu 430	Asp
ggc cgt att gaa Gly Arg lle Glu 435	Val Glu Ihr Pr	ca aat gaa gcg ro Asn Glu Ala 40	acc att gtc ata Thr lie Val lle 445	gaa 1344 Glu
cgt caa aat aaa Arg Gin Asn Lys 450		is lle Ala Thr		
caa gat atg aca Gin Asp Met Thr 465				
gaa Glu				1443

<400> 2

Met Pro lie Thr Asn Lys Thr Met Leu lie Thr Tyr Ala Asp Ser Leu 1 5 10 15

<210> 2 <211> 481 <212> PRT <213> Streptococcus mutans

EGO14US-Sequence Listing.txt Page

Gly Lys Asn Leu Lys Glu Leu Asn Glu Asn lie Glu Asn Tyr Phe Gly $20 \hspace{1cm} 25 \hspace{1cm} 30$

Asp Ala Val Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly 35 40 45

Asp Arg Gly Phe Ala Pro IIe Asp Tyr His Glu Val Asp Ser Ala Phe 50 55 60

Gly Asp Trp Asp Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met 65 70 75 80

Phe Asp Phe Met 11e Asn His IIe Ser Arg Gln Ser Lys Tyr Tyr Lys $85 \hspace{0.5cm} 90 \hspace{0.5cm} 95$

Asp Tyr Gln Glu Lys His Glu Ala Ser Ala Tyr Lys Asp Leu Phe Leu 100 105 110

Asn Trp Asp Lys Phe Trp Pro Lys Asn Arg Pro Thr Gln Glu Asp Val

Asp Leu lie Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gin Giu lie Gin 130 140

Phe Ala Asp Gly Ser Val Glu His Leu Trp Asn Thr Phe Gly Glu Glu 145 150 155 160

Gin IIe Asp Leu Asp Val Thr Lys Giu Val Thr Met Asp Phe IIe Arg 165 170 175

Ser Thr lie Giu Asn Leu Aia Aia Asn Giy Cys Asp Leu lie Arg Leu 180 185 190

Asp Ala Phe Ala Tyr Ala Val Lys Leu Asp Thr Asn Asp Phe Phe 195 200 205

Val Glu Pro Glu ile Trp Thr Leu Leu Asp Lys Val Arg Asp ile Ala 210 215 220

Ala Val Ser Gly Ala Glu IIe Leu Pro Glu IIe His Glu His Tyr Thr 225 230 235 240

lle Gin Phe Lys Ile Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala 245 250 255

Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Val Asp Arg 260 265 270

Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gin Phe Thr Thr Leu 275 280 285

Asp Thr His Asp Gly IIe Gly Val Val Asp Val Lys Asp IIe Leu Thr 290 295 300

Asp Glu Glu IIe Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Vai Gly Ala 305 310 320

Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp Ile 325 330 335

Tyr Gin lie Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Gin 340 345

EG014US-Sequence Listing.txt Lys Tyr Phe Leu Ala Arg Leu ile Gin Ala Phe Ala Pro Gly ile Pro 355 360 365 Gin Vai Tyr Tyr Vai Gly Phe Leu Ala Gly Lys Asn Asp Leu Glu Leu 370 375 380 Leu Glu Ser Thr Lys Glu Gly Arg Asn IIe Asn Arg His Tyr Tyr Ser 385 390 395 400 Ser Giu Giu ile Ala Lys Giu Val Lys Arg Pro Val Val Lys Ala Leu 405 410 415 Leu Asn Leu Phe Thr Tyr Arg Asn Gln Ser Ala Ala Phe Asp Leu Asp 420 425 430 Gly Arg lie Glu Val Glu Thr Pro Asn Glu Ala Thr lie Val ile Glu 435 440 445 Arg Gin Asn Lys Asp Gly Ser His IIe Ala Thr Ala Glu IIe Asn Leu 450 455 460 Gin Asp Met Thr Tyr Arg Val Thr Giu Asn Asp Gin Thr Ile Ser Phe 465 470 475 480 Glu <210> 3 <211> 1434 <212> DNA <213> Strep Streptococcus pneumoniae <220> <221> CDS <222> (1)..(1434) atg cca att caa aat aaa acc atg ttg att acc tat tct gat agc ctt Met Pro Ile Gin Asn Lys Thr Met Leu Ile Thr Tyr Ser Asp Ser Leu 1 5 10 15 96 gga aat aat ctt aaa gac tta tat gat aat ttg gaa gag cat ttt gga Gly Asn Asn Leu Lys Asp Leu Tyr Asp Asn Leu Glu Glu His Phe Gly 20 25 30 gat gct att gga gga gtt cac ctt tta cca ttt ttc cca tca aca gtt Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Val 35 40 45 144 192 gat cgt gga ttt gcg cca gtt gac tac gac gaa gtg gac tca gct ttt Asp Arg Gly Phe Ala Pro Val Asp Tyr Asp Glu Val Asp Ser Ala Phe 50 55 ggt gat tgg gag gat gtg aag cgt tta ggt gag aaa tat tat ctt atg Gly Asp Trp Glu Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met 65 70 75 80 240 ttt gat ttt atg att aat cat att tct cgt caa tcc aag tat tat aag Phe Asp Phe Met IIe Asn His IIe Ser Arg Gln Ser Lys Tyr Tyr Lys 85 90 95 gac tat caa gaa aaa cat gaa gcc agt gaa ttt aaa gct ctc ttt tta Asp Tyr Gln Glu Lys His Glu Ala Ser Glu Phe Lys Ala Leu Phe Leu 100 105 110 336 aac tgg gat aag ttt tgg cca gaa aac cgt ccg aca cag tct gat gta Asn Trp Asp Lys Phe Trp Pro Glu Asn Arg Pro Thr Gln Ser Asp Val 115 120 125 384

gat tta att tac aag cgt aag gat cgt gca cca aag caa gag att gtg Asp Leu lie Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gin Glu lie Vali 130 135 140

ttt gaa gat ggt tca gtg gaa cat ttg tgg aat acc ttt ggt gag gag Phe Glu Asp Gly Ser Val Glu His Leu Trp Asn Thr Phe Gly Glu Glu 432

480

EG014US-Sequenc	e Listing.txt	Page 5		
145	150	155		160
cag att gat ctt Gin lie Asp Leu	gat gtg acc aaa Asp Val Thr Lys 165	a gaa gta act s Glu Val Thr 170	Met Glu Phe	atc cgt 528 lle Arg 175
	g cac ttg gca agt n His Leu Ala Ser)			
	tat gca gtg aag Tyr Ala Val Lys 200	s Lys Leu Asp		
gtg gaa cca gat Val Glu Pro Asp 210	t att tgg gat tta o lle Trp Asp Leu 215	a ttg gac aaa u Leu Asp Lys	gtt cga gat Val Arg Asp 220	atc gct 672 lie Ala
	g aca gag ctt tta 7 Thr Glu Leu Leu 230		His Glu His	
	a ata gca gac cat i lle Ala Asp His 245		Val Tyr Asp	
	g aca ctt tat act Thr Leu Tyr Thi			
	g tta aag atg ago D Leu Lys Met Sei 280	r Pro Met Lys		
	t ggg att gga gta o Gly lle Gly Val 295			
	t gac tat gct tca e Asp Tyr Ala Sei 310		Tyr Lys Val	
aat gtc aaa cgi Asn Val Lys Arg	t aag tac tot agg g Lys Tyr Ser Ser 325	t gcc gag tat r Ala Glu Tyr 330	Asn Asn Leu	gat atc 1008 Asp lle 335
	t tca acc tac ta n Ser Thr Tyr Tyr)			
	gct cgt cta att Ala Arg Leu IIe 360	e Gin Ala Phe		
cag att tac tat Gin lie Tyr Tyr 370	t gtg ggt cta tta Val Gly Leu Leu 375	a gca ggc aag u Ala Giy Lys	aat gac ttg Asn Asp Leu 380	aaa tta 1152 Lys Leu
	t aaa gaa ggt cga Lys Glu Gly Arg 390		Arg His Tyr	
aac gag gaa ata Asn Glu Glu Ile	n gca aaa gaa gtg e Ala Lys Glu Val 405	g caa cga cct I GIn Arg Pro 410	Val Val Lys	gcc ctt 1248 Ala Leu 415
	t tot tto ogt aad Ser Phe Arg Ass)			
ggg act act gag Gly Thr Thr Glu 435	g ata gag aca cca ı ile Giu Thr Pro 440	o Thr Ala His	agc att gta Ser lle Val 445	atc aaa 1344 lle Lys
cgt caa aat aas Arg Gin Asn Lys 450	a gat aag too gta s Asp Lys Ser Val 455	a aca gca gta I Thr Ala Val	gta gaa att Val Glu lle 460	gat ttg 1392 Asp Leu
caa aat cag act Gin Asn Gin Thi 465	t tat cgg gta att Tyr Arg Val 116 470	t gag aat gga e Glu Asn Gly 475	Val Glu Val	1434

EG014US-Sequence Listing.txt

<212> PRT
<213> Streptococcus pneumoniae

Met Pro IIe Gin Asn Lys Thr Met Leu IIe Thr Tyr Ser Asp Ser Leu 1 5 10 15

Gly Asn Asn Leu Lys Asp Leu Tyr Asp Asn Leu Glu Glu His Phe Gly 20 25 30

Asp Ala 11e Gly Gly Val His Leu Leu Pro Phe Pro Ser Thr Val $35 \ \ \, 40 \ \ \, 45$

Asp Arg Gly Phe Ala Pro Val Asp Tyr Asp Glu Val Asp Ser Ala Phe 50 60

Gly Asp Trp Glu Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met 65 70 75 80

Phe Asp Phe Met IIe Asn His IIe Ser Arg Gln Ser Lys Tyr Tyr Lys 85 90 95

Asp Tyr Gln Glu Lys His Glu Ala Ser Glu Phe Lys Ala Leu Phe Leu 100 105 110

Asn Trp Asp Lys Phe Trp Pro Giu Asn Arg Pro Thr Gin Ser Asp Val 115 120 125

Asp Leu lie Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gin Glu lie Val

Phe Glu Asp Gly Ser Val Glu His Leu Trp Asn Thr Phe Gly Glu Glu 145 150 155 160

Gin lie Asp Leu Asp Val Thr Lys Glu Val Thr Met Giu Phe lie Arg 165 170 175

Lys Thr lie Gin His Leu Ala Ser Asn Gly Cys Asp Leu Ile Arg Leu 180 185 190

Asp Ala Phe Ala Tyr Ala Val Lys Leu Asp Thr Asn Asp Phe Phe 195 200 205

Val Glu Pro Asp Ile Trp Asp Leu Leu Asp Lys Val Arg Asp Ile Ala 210 215 220

Ala Glu Tyr Gly Thr Glu Leu Leu Pro Glu Ile His Glu His Tyr Ser 225 230 235 240

lle Gin Phe Lys lle Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala 245 250 255

Leu Pro Met Val Thr Leu Tyr Thr Leu Tyr Ser Ser Arg Thr Glu Arg 260 265 270

Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gin Phe Thr Thr Leu 275 280 285

Asp Thr His Asp Gly IIe Gly Val Val Asp Val Lys Asp IIe Leu Thr 290 295 300

Asp Glu Glu lle Asp Tyr Ala Ser Asn Glu Leu Tyr Lys Val Gly Ala 305 310 320

EG014US-Sequence Listing.txt Asn Val Lys Arg Lys Tyr Ser Ser Ala Glu Tyr Asn Asn Leu Asp 11e 325 330 335 Tyr Gin ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Val Lys Tyr Phe Leu Ala Arg Leu Ile Gin Ala Phe Ala Pro Gly Ile Pro 355 360 365 Gin lie Tyr Tyr Val Gly Leu Leu Ala Gly Lys Asn Asp Leu Lys Leu 370 375 380 Leu Glu Glu Thr Lys Glu Gly Arg Asn IIe Asn Arg His Tyr Tyr Ser 385 390 395 400 Asn Giu Giu ile Ala Lys Giu Val Gin Arg Pro Val Val Lys Ala Leu 405 410 415 Leu Asn Leu Phe Ser Phe Arg Asn Arg Ser Glu Ala Phe Asp Leu Glu 420 425 430 Gly Thr Thr Glu lie Glu Thr Pro Thr Ala His Ser lie Val lie Lys 435 440 445 Arg Gin Asn Lys Asp Lys Ser Vai Thr Ala Val Val Glu ile Asp Leu 450 460 Gin Asn Gin Thr Tyr Arg Val Ile Giu Asn Giy Val Giu Val 465 470 475 <210> 5
<211> 1443
<212> DNA
<213> Strep Streptococcus sorbinus <220> <221> CDS <222> (1)..(1443) **<400>** 5 atg aca cta aca aat aaa acg atg tta att acc tac tca gat agt tta Met Thr Leu Thr Asn Lys Thr Met Leu IIe Thr Tyr Ser Asp Ser Leu 1 5 10 15 ggt agg aac cta aaa gag ctg gat gaa aat atc agc atc tat ttt gga Gly Arg Asn Leu Lys Glu Leu Asp Glu Asn Ile Ser Ile Tyr Phe Gly 20 25 30 96 gat gca att gga ggc gtc cat ctc ctg cct ttc ttc ccc tcg aca gga Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly 35 40 45 144 gat agg gga ttc gct cca gtt gat tac gat aag gtg gat cct gct ttt Asp Arg Gly Phe Ala Pro Val Asp Tyr Asp Lys Val Asp Pro Ala Phe 50 55 60 192 240 ggt gac tgg gat gat gtc aaa cgt tta ggt gct aaa tac tac ctg atg Gly Asp Trp Asp Asp Val Lys Arg Leu Gly Ala Lys Tyr Tyr Leu Met 65 70 80 ttt gat ttt atg att aat cat atc tcc cgt caa tct aag tat tat aag Phe Asp Phe Met IIe Asn His IIe Ser Arg Gln Ser Lys Tyr Tyr Lys 85 90 95 288 gat ttt caa gag aaa aaa gat gct tct gac tat gcg gat tta ttt ctg Asp Phe Gin Giu Lys Lys Asp Ala Ser Asp Tyr Ala Asp Leu Phe Leu 100 105 110 336 cgc tgg gaa aaa ttc tgg ccg gaa aac cgt ccc acc caa gca gat att Arg Trp Glu Lys Phe Trp Pro Glu Asn Arg Pro Thr Gln Ala Asp Ile 115 120 125

gat tta att tat aaa cgt aaa gac aag gct cct atg cag gag att gtc Asp Leu lie Tyr Lys Arg Lys Asp Lys Ala Pro Met Gin Glu lie Val 432

Luo	400	o c q	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,			5	•		,, ,							
	130					135					140					
ttc Phe 145	gcc Ala	gat Asp	gga Gly	acc Thr	aaa Lys 150	gaa Glu	cat His	c t c Leu	tgg Trp	aat Asn 155	act Thr	ttc Phe	gga Gly	gaa Glu	gag Glu 160	480
						act Thr										528
						gca Ala										576
						gtg Val										624
gtc Val	gaa Glu 210	cca Pro	gaa Glu	att	tgg Trp	gat Asp 215	c t c Leu	cta Leu	acc Thr	aag Lys	gta Val 220	cag Gln	aca Thr	atc Ile	gcc Ala	672
aag Lys 225	gaa Glu	gca Ala	ggg Gly	gca Ala	gat Asp 230	atc lie	ctg Leu	ccg Pro	gaa Glu	ata Ile 235	cat His	gag Glu	cat His	tat Tyr	tct Ser 240	720
atc Ile	cag Gin	ttc Phe	aaa Lys	att IIe 245	gc t Ala	gag Glu	cat His	gac Asp	tat Tyr 250	ttc Phe	att	tat Tyr	gat Asp	ttt Phe 255	gcc Ala	768
ctt Leu	cca Pro	atg Met	gta Vai 260	acc Thr	ctt Leu	tac Tyr	tct Ser	ctt Leu 265	tat Tyr	agc Ser	ggt Gly	agg Arg	gtg Val 270	caa Gin	cgt Arg	816
t tg Leu	gca Ala	gat Asp 275	tgg Trp	ctg Leu	gct Ala	aaa Lys	agt Ser 280	cct Pro	atg Met	aag Lys	caa Gin	ttt Phe 285	act Thr	acg Thr	ctg Leu	864
						gga Gly 295										912
gac Asp 305	gag Glu	gaa Glu	att Ile	gc t Ala	tac Tyr 310	act Thr	tcc Ser	gat Asp	caa Gin	ctc Leu 315	tac Tyr	aag Lys	gtt Val	gga Gly	gcc Ala 320	960
						tca Ser										1008
						tac Tyr										1056
						c t c Leu										1104
caa Gin	gtt Val 370	tat Tyr	tat Tyr	gtt Val	gga Gly	ctt Leu 375	t t g Leu	gc t Ala	gga Gly	aaa Lys	aac Asn 380	gat Asp	ctg Leu	aag Lys	ctc Leu	1152
						ggt Gly										1200
						gag Glu										1248
						cgc Arg										1296
						gtt Val										1344
						agt Ser 455										1392
						gtc Val										1440

gaa Glu

<210> 6

(2112 481 (212) PRT

(213) Streptococcus sorbinus

<400> 6

Met Thr Leu Thr Asn Lys Thr Met Leu lie Thr Tyr Ser Asp Ser Leu 1 5 10 15

Page 9

Gly Arg Asn Leu Lys Glu Leu Asp Glu Asn lie Ser lie Tyr Phe Gly 20 25 30

Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly 35 40 45

Asp Arg Gly Phe Ala Pro Val Asp Tyr Asp Lys Val Asp Pro Ala Phe 50 60

Gly Asp Trp Asp Asp Val Lys Arg Leu Gly Ala Lys Tyr Tyr Leu Met 65 70 75 80

Phe Asp Phe Met lie Asn His IIe Ser Arg Gln Ser Lys Tyr Tyr Lys 85 90 95

Asp Phe Gin Giu Lys Lys Asp Ala Ser Asp Tyr Aia Asp Leu Phe Leu 100 105 110

Arg Trp Glu Lys Phe Trp Pro Glu Asn Arg Pro Thr Gln Ala Asp Ile 115 120 125

Asp Leu lie Tyr Lys Arg Lys Asp Lys Ala Pro Met Gin Giu lie Val 130 135 140

Phe Ala Asp Gly Thr Lys Glu His Leu Trp Asn Thr Phe Gly Glu Glu 145 150 155 160

Gin ile Asp Leu Asp Val Thr Lys Giu Vai Thr Met Asp Phe ile Lys 165 170 175

Lys Asn Ile Glu His Leu Ala Val Asn Gly Cys Asp Leu Ile Arg Leu 180 185 190

Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe 195 200 205

Val Glu Pro Glu Ile Trp Asp Leu Leu Thr Lys Val Gln Thr Ile Ala 210 215 220

Lys Glu Ala Gly Ala Asp lle Leu Pro Glu Ile His Glu His Tyr Ser 225 230 235 240

lle Gin Phe Lys Ile Ala Giu His Asp Tyr Phe Ile Tyr Asp Phe Ala 245 250 255

Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Arg Val Gin Arg 260 270

Leu Ala Asp Trp Leu Ala Lys Ser Pro Met Lys Gln Phe Thr Thr Leu 275 280 285

<210>	7	
(211)	1470	
〈212〉	DNA	
〈213〉	Leuconostoc	mesenteroides

<220> <221> CDS <222> (1)..(1470)

EG0	EGO14US-Sequence Listing.txt Page 11															
				85					90					95		
gat Asp	ttt Phe	aag Lys	aag Lys 100	aa t As n	cat His	gac Asp	gat Asp	tca Ser 105	aag Lys	tat Tyr	aaa Lys	gat Asp	ttc Phe 110	ttt Phe	att ile	336
cgt Arg	tgg Trp	gaa Glu 115	aag Lys	ttc Phe	tgg Trp	gca Ala	aag Lys 120	gcc Ala	ggc Gly	gaa Glu	aac Asn	cgt Arg 125	cca Pro	aca Thr	caa Gin	384
					att											432
gaa Glu 145	atc ile	act Thr	ttt Phe	gat Asp	gat Asp 150	ggc Gly	aca Thr	aca Thr	gaa Glu	aac Asn 155	t t g Leu	tgg Trp	aat Asn	act Thr	ttt Phe 160	480
ggt Gly	gaa Glu	gaa Glu	caa Gln	att ile 165	gac Asp	att	gat Asp	gtt Val	aat Asn 170	tca Ser	gcc Ala	att	gcc Ala	aag Lys 175	gaa Glu	528
					ctt Leu											576
					ttt Phe											624
					cca Pro											672
					tta Leu 230											720
					aaa Lys											768
					atg Met											816
aca Thr	aa t As n	caa Gln 275	ttg Leu	gca Ala	aag Lys	tgg Trp	ttg Leu 280	aag Lys	atg Met	tca Ser	cca Pro	atg Met 285	aag Lys	caa Gin	t t c Phe	864
					cat His											912
11e 305	Leu	Thr	Asp	Asp	gaa Glu 310	Пe	Asp	Tyr	Ala	Ser 315	Glu	Gin	Leu	Tyr	Lys 320	960
Val	Gly	Ala	Asn	Val 325	aaa Lys	Lys	Thr	Tyr	Ser 330	Ser	Ala	Ser	Tyr	Asn 335	Asn	1008
Leu	Asp	He	Tyr 340	GIn	att Ile	Asn	Ser	Thr 345	Tyr	Tyr	Ser	Ala	150 350	Gly	Asn	1056
gat Asp	ga t Asp	gca Ala 355	gca Ala	tac Tyr	t t g Leu	t t g Leu	agt Ser 360	cgt Arg	gtc Val	t t c Phe	caa Gin	gtc Val 365	ttt Phe	gcg Ala	cct Pro	1104
gga Gly	att 1 e 370	cca Pro	caa Gln	att	tat Tyr	tac Tyr 375	gtt Val	ggt Gly	ttg Leu	t t g Leu	gca Ala 380	gg t Gly	gaa Glu	aac Asn	ga t Asp	1152
11e 385	Ala	Leu	Leu	Glu	tca Ser 390	Thr	Lys	Glu	Gly	Arg 395	Asn	lle	Asn	Arg	His 400	1200
tac Tyr	tat Tyr	acg Thr	cgt Arg	gaa Glu 405	gaa Glu	gtt Val	aag Lys	tca Ser	gaa Glu 410	gtt Val	aag Lys	cga Arg	cca Pro	gtt Vai 415	gt t Val	1248 [.]
gc t Ala	aac Asn	tta Leu	ttg Leu 420	aag Lys	cta Leu	ttg Leu	tca Ser	tgg Trp 425	cgt Arg	aat Asn	gaa Glu	agc Ser	cct Pro 430	gca Ala	ttt Phe	1296

EG014US-Sequence	Listing txt	Page 12
CG01403~3600611ce	FISCING. INC	IABOIL

gat Asp	ttg Leu	gct Ala 435	gg¢ Gly	tca Ser	atc lie	aca Thr	gtt Val 440	gac Asp	acg Thr	cca Pro	act Thr	gat Asp 445	aca Thr	aca Thr	att lle	1344
														tta Leu		1392
														caa Gln		1440
	atg Met															1470

(211) 49(

<213> Leuconostoc mesenteroides

<400> 8

Met Glu lie Gln Asn Lys Ala Met Leu lie Thr Tyr Ala Asp Ser Leu 1 10 15

Gly Lys Asn Leu Lys Asp Val His Gln Val Leu Lys Glu Asp Ile Gly 20 25 30

Asp Ala Ite Giy Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly $35 \ \ \, 40 \ \ \, 45$

Asp Arg Gly Phe Ala Pro Ala Asp Tyr Thr Arg Val Asp Ala Ala Phe $50 55 60$

Gly Asp Trp Ala Asp Val Glu Ala Leu Gly Glu Glu Tyr Tyr Leu Met 65 70 75 80

Phe Asp Phe Met IIe Asn His 11e Ser Arg Glu Ser Val Met Tyr Gln 85 90 95

Asp Phe Lys Lys Asn His Asp Asp Ser Lys Tyr Lys Asp Phe Phe 11e 100 105 110

Arg Trp Glu Lys Phe Trp Ala Lys Ala Gly Glu Asn Arg Pro Thr Gln 115 120 125

Ala Asp Val Asp Leu lle Tyr Lys Arg Lys Asp Lys Ala Pro Thr Gln 130 135 140

Glu lle Thr Phe Asp Asp Gly Thr Thr Glu Asn Leu Trp Asn Thr Phe 145 150 155 160

Gly Glu Glu Gln lle Asp lle Asp Val Asn Ser Ala lle Ala Lys Glu 165 170 175

Phe lle Lys Thr Thr Leu Glu Asp Met Val Lys His Gly Ala Asn Leu 180 185 190

lie Arg Leu Asp Ala Phe Ala Tyr Ala Val Lys Lys Val Asp Thr Asn 195 200 205

Asp Phe Phe Val Glu Pro Glu lle Trp Asp Thr Leu Asn Glu Val Arg 210 215 220

Glu lle Leu Thr Pro Leu Lys Ala Glu lle Leu Pro Glu lle His Glu 225 230 235 240 EG014US-Sequence Listing.txt

His Tyr Ser lle Pro Lys Lys lle Asn Asp His Gly Tyr Phe Thr Tyr 245 250 255

Asp Phe Ala Leu Pro Met Thr Thr Leu Tyr Thr Leu Tyr Ser Gly Lys 260 265 270

Thr Asn Gin Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gin Phe 275 280 285

Thr Thr Leu Asp Thr His Asp Gly Ile Gly Val Val Asp Ala Arg Asp 290 295 300

lie Leu Thr Asp Asp Giu lie Asp Tyr Ala Ser Giu Gin Leu Tyr Lys 305 310 315 320

Val Gly Ala Asn Val Lys Lys Thr Tyr Ser Ser Ala Ser Tyr Asn Asn 325 330 335

Leu Asp lie Tyr Gin Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asn 340 350

Asp Asp Ala Ala Tyr Leu Leu Ser Arg Val Phe Gln Val Phe Ala Pro 355 360 365

Gly lie Pro Gin lie Tyr Tyr Val Gly Leu Leu Ala Gly Glu Asn Asp 370 375 380

lle Ala Leu Leu Glu Ser Thr Lys Glu Gly Arg Asn lle Asn Arg His 385 390 395 400

Tyr Tyr Thr Arg Glu Glu Val Lys Ser Glu Val Lys Arg Pro Val Val 405 410 415

Ala Asn Leu Leu Lys Leu Leu Ser Trp Arg Asn Glu Ser Pro Ala Phe 420 425 430

Asp Leu Ala Gly Ser lie Thr Val Asp Thr Pro Thr Asp Thr Thr lie 435 440 445

Val Val Thr Arg Gin Asp Giu Asn Giy Gin Asn Lys Ala Val Leu Thr 450 455 460

Ala Asp Ala Ala Asn Lys Thr Phe Glu lie Val Glu Asn Gly Gln Thr 465 470 475 480

Val Met Ser Ser Asp Asn Leu Thr Gln Asn 485 490

<210> 9 <211> 1467 <212> DNA <213> Oenococcus oeni

<220> <221> CDS <222> (1)..(1467)

atg ccg gtt aaa aat aaa gca atg ctg atc acc tat tcg gat tcg atg Met Pro Val Lys Asn Lys Ala Met Leu lie Thr Tyr Ser Asp Ser Met 1 10 15

ggt aag aat atc aag gaa tta caa tac att tta gat aaa tat att gga Gly Lys Asn lie Lys Glu Leu Gin Tyr lie Leu Asp Lys Tyr lie Gly 20 25 30

gac gcg att ggt gga gtt cat ctg ctg cct ttt ttt ccg tca acc gga Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly

EGUI	405-	Sequ	ence	LIS	ting	. tx t		гав	e 14	•						
		35					40					45				
ga t Asp	cgt Arg 50	ggt Gly	ttt Phe	gcg Ala	ccc Pro	teg Ser 55	ga t Asp	tac Tyr	act Thr	cgt Arg	gtc Val 60	aat Asn	ccg Pro	gat Asp	ttc Phe	192
ggt Gly 65	gat Asp	tgg Trp	gag Glu	gat Asp	gtc Val 70	gag Glu	gaa Glu	ctt Leu	gga Gly	aaa Lys 75	aag Lys	tat Tyr	tat Tyr	tta Leu	atg Met 80	240
ttt Phe	gat Asp	ttc Phe	atg Met	att Ile 85	aat Asn	cac His	att	tcc Ser	cgt Arg 90	gaa Glu	tcg Ser	att	atg Met	tat Tyr 95	caa Gin	288
gat Asp	ttc Phe	aag Lys	gaa Glu 100	aaa Lys	aag Lys	gat Asp	gct Ala	tcc Ser 105	agc Ser	tac Tyr	aag Lys	gac Asp	ttt Phe 110	ttt Phe	att lie	336
cgt Arg	tgg Trp	gaa Glu 115	aag Lys	ttc Phe	tgg Trp	ccg Pro	aaa Lys 120	gga Gly	cgc Arg	ccg Pro	acg Thr	aag Lys 125	gcc Ala	ga t Asp	atc ile	384
gat Asp	tta Leu 130	att	tac Tyr	aaa Lys	aga Arg	aaa Lys 135	gat Asp	aag Lys	gcg Ala	ccg Pro	att lle 140	cag Gln	ggg Gly	att ile	act Thr	432
ttt Phe 145	gca Ala	gac Asp	ggc Gly	agt Ser	caa Gin 150	gaa Glu	cat His	ctt Leu	tgg Trp	aat Asn 155	act Thr	ttt Phe	ggc Gly	ga t Asp	gag Glu 160	480
cag Gin	atc lle	gat Asp	att lie	aac Asn 165	gtg Val	aag Lys	tcc Ser	aaa Lys	gtt Val 170	gc t Ala	cag Gin	gaa Glu	ttt Phe	ttt Phe 175	aaa Lys	528
gat Asp	act Thr	tta Leu	cag Gin 180	tca Ser	atg Met	gtt Val	aag Lys	cac His 185	gg t Gly	gcg Ala	gat Asp	ttg Leu	att Ile 190	cgc Arg	ctg Leu	576
gat Asp	gcc Ala	ttt Phe 195	gct Ala	tat Tyr	gca Ala	att	aaa Lys 200	aag Lys	att lie	gat Asp	act Thr	aat Asn 205	gac Asp	ttc Phe	ttt Phe	624
att	gaa Glu 210	ccg Pro	gaa Glu	att	tgg Trp	gat Asp 215	tta Leu	ctg Leu	gaa Glu	tca Ser	gtt Val 220	cgg Arg	aag Lys	att He	ctc Leu	672
gac Asp 225	ccc Pro	cta Leu	cat His	gc t Ala	gaa Glu 230	att lie	t ta Leu	ccg Pro	gaa Glu	att 11e 235	tat Tyr	gaa Glu	cat His	tac Tyr	aca Thr 240	720
a t c I I e	ccg Pro	gcc Ala	aaa Lys	ata Ile 245	aat Asn	gag Glu	tat Tyr	gg t Gly	tac Tyr 250	ttt Phe	acc Thr	tat Tyr	gat Asp	ttt Phe 255	gtt Val	768
t t a Leu	cct Pro	c t g Leu	gta Val 260	lle	t tg Leu	tac Tyr	act Thr	ctt Leu 265	tat Tyr	tct Ser	gga Gly	aat Asn	Pro 270	aag Lys	caa Gin	816
Leu	Ala	Lys 275	Trp	Leu	aaa Lys	Met	Ser 280	Pro	Lys	Lys	Gin	Phe 285	Thr	Thr	Leu	864
	290				atc Ile	295					300					912
Asp 305	Glu	Glu	lle	Asp	tat Tyr 310	Thr	Ser	Ser	Glu	115 315	Tyr	Lys	Val	Gly	320	960
Asn	Val	Lys	Arg	Thr 325		Ser	Ser	Ala	330	Tyr	Asn	Asn	Leu	335	116	1008
Tyr	Gin	lle	Asn 340	Ser	acc Thr	Tyr	Tyr	Ser 345	Ala	Leu	Gly	Asn	350	ASP	Lys	1056
Ala	Tyr	Leu 355	Leu	Ala	cgt Arg	Ala	360	Gin	lle	Phe	Ala	Pro 365	Gly	116	Pro	1104
caa Gln	atc 11e 370	Tyr	tac Tyr	gca	ggc Gly	ctg Leu 375	Leu	gct Ala	gg t Gly	gaa Glu	aac Asn 380	Asp	t t g Leu	ga t Asp	t t g Leu	1152

EG014US-Sequence Listing.txt Page 15

EGU	1405-	-Sequ	ience	2 E I S	ting	ζ. ι χι		ган	ge it)						
t tg Leu 385	gaa Glu	aag Lys	acc Thr	aag Lys	gaa Giu 390	gga Gly	cgc Arg	aa t As n	ata Ile	aat Asn 395	cgt Arg	cat His	tat Tyr	tac Tyr	agt Ser 400	1200
gaa Glu	gaa Glu	gaa Glu	gtt Val	gcc Ala 405	aat Asn	gaa Glu	gtg Val	cag Gin	aga Arg 410	cca Pro	att He	gtt Val	gcc Ala	tgc Cys 415	cta Leu	1248
c t g L e u	aaa Lys	ttg Leu	ttg Leu 420	gct Ala	tgg Trp	cgc Arg	aat Asn	cgc Arg 425	agt Ser	gcc Ala	gc t Ala	ttt Phe	gat Asp 430	ctt Leu	caa Gln	1296
gga Gly	gat Asp	att lle 435	caa Gln	gtc Val	agc Ser	gca Ala	acc Thr 440	gac Asp	aaa Lys	aat Asn	gaa Glu	atc Ile 445	aaa Lys	att He	att He	1344
cga Arg	act Thr 450	tca Ser	acc Thr	aat Asn	ggc Gly	caa Gln 455	gac Asp	acc Thr	gcg Ala	gaa Glu	tta Leu 460	acc Thr	gct Ala	aat Asn	gtg Val	1392
gct Ala 465	Leu	aaa Lys	acc Thr	ttt Phe	act Thr 470	ata Ile	aag Lys	gaa Glu	aat Asn	gat Asp 475	aaa Lys	att lie	att He	tta Leu	att He 480	1440
gaa Glu	gat Asp	cag Gln	act Thr	gat Asp 485	aca Thr	aag Lys	gat Asp	atc Ile								1467
<21 <21 <21 <21	1> 2>	10 489 PRT Oeno	COCCI	ús o	eni											
<40	0>	10														
Met 1	Pro	Val	Lys	Asn 5	Lys	Ala	Met	Leu	e 10	Thr	Tyr	Ser	Asp	Ser 15	Met	
Gly	Lys	Asn	11e 20	Lys	Glu	Leu	GIn	Tyr 25	He	Leu	Asp	Lys	Tyr 30	lle	Gly	
Asp	Ala	11e 35	Gly	Gly	Vai	His	Leu 40	Leu	Pro	Phe	Phe	Pro 45	Ser	Thr	Gly	
Asp	Arg 50	Gly	Phe	Ala	Pro	Ser 55	Asp	Tyr	Thr	Arg	Val 60	Asn	Pro	Asp	Phe	
G I y 65	Asp	Trp	Glu	Asp	Va I 70	Glu	Glu	Leu	Gly	Lys 75	Lys	Tyr	Tyr	Leu	Met 80	
Phe	Asp	Phe	Met	11e 85	Asn	His	lle	Ser	Arg 90	Glu	Ser	lle	Met	Tyr 95	Gln	
Asp	Phe	Lys	G! u 100	Lys	Lys	Asp	Ala	Ser 105		Tyr	Lys	Asp	Phe 110	Phe	lle	
Arg	Trp	Glu 115		Phe	Trp	Pro	Lys 120		Arg	Pro	Thr	Lys 125	Ala	Asp	He	
Asp	130		Tyr	Lys	Arg	Lys 135		Lys	Ala	Pro	11e 140		Gly	ile	Thr	
145	i			Ser	150					155					160	
Glr	ı ile	: Asp	lle	Asn 165		Lys	Ser	Lys	Val 170	Ala	GIn	Glu	Phe	Phe 175	Lys	
Asp	Thr	Leu	GIn 180	Ser	Met	Val	Lys	His 185		Ala	Asp	Leu	11e 190	Arg	Leu	

EG014US-Sequence Listing.txt Page 16

Asp Ala Phe Ala Tyr Ala lle Lys Lys lle Asp Thr Asn Asp Phe Phe 195 200 205

lle Glu Pro Glu lle Trp Asp Leu Leu Glu Ser Val Arg Lys lle Leu 210 215 220

Asp Pro Leu His Ala Glu lle Leu Pro Glu lle Tyr Glu His Tyr Thr 225 230 235 240

lle Pro Ala Lys lle Asn Glu Tyr Gly Tyr Phe Thr Tyr Asp Phe Val 245 250 255

Leu Pro Leu Val IIe Leu Tyr Thr Leu Tyr Ser Gly Asn Pro Lys Gln 260 265 270

Leu Ala Lys Trp Leu Lys Met Ser Pro Lys Lys Gln Phe Thr Thr Leu 275 280 285

Asp Thr His Asp Gly lie Gly Val Val Asp Ala Arg Asp IIe Leu Thr 290 295 300

Asp Glu Glu lle Asp Tyr Thr Ser Ser Glu Leu Tyr Lys Val Gly Ala 305 310 315 320

Asn Val Lys Arg Thr Tyr Ser Ser Ala Ala Tyr Asn Asn Leu Asp lle 325 330 335

Tyr Gin lie Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asn Asp Asp Lys 340 345 350

Ala Tyr Leu Leu Ala Arg Ala lle Gln lle Phe Ala Pro Gly lle Pro 355 360 365

Gin ile Tyr Tyr Ala Giy Leu Leu Ala Giy Giu Asn Asp Leu Asp Leu 370 380

Leu Glu Lys Thr Lys Glu Gly Arg Asn Ite Asn Arg His Tyr Tyr Ser 385 390 395 400

Giu Giu Vai Ala Asn Glu Vai Gin Arg Pro 11e Vai Ala Cys Leu 405 410 415

Leu Lys Leu Leu Ala Trp Arg Asn Arg Ser Ala Ala Phe Asp Leu Gin 420 425 430

Gly Asp lie Gin Val Ser Ala Thr Asp Lys Asn Glu ile Lys lie lie 435 440 445

Arg Thr Ser Thr Asn Gly Gln Asp Thr Ala Glu Leu Thr Ala Asn Val 450 455

Ala Leu Lys Thr Phe Thr lle Lys Glu Asn Asp Lys lle lle Leu lle 465 470 475 480

Glu Asp Gin Thr Asp Thr Lys Asp lle 485

<210> 11
<211> 1446
<212> DNA
<213> Streptococcus mitis

(220) (221) CDS (222) (1)..(1446)

<400																
atg Met 1	cca Pro	att	cag Gln	aat Asn 5	aaa Lys	acc Thr	atg Met	t t g Leu	att ile 10	acc Thr	tat Tyr	tca Ser	ga t Asp	agt Ser 15	c t g Leu	48
gga Gly	aat Asn	aa t Asn	ctt Leu 20	aaa Lys	gac Asp	tta Leu	tat Tyr	gag Glu 25	aat Asn	ttg Leu	gaa Glu	gag Glu	tat Tyr 30	ttt Phe	gga Gly	96
gat Asp	gct Ala	att 11e 35	ggg Gly	gga Gly	gtt Val	cac His	ctt Leu 40	cta Leu	cca Pro	ttt Phe	t t c Phe	cca Pro 45	tca Ser	aca Thr	gg t Gly	144
								tac Tyr								192
ggt Gly 65	gat Asp	tgg Trp	gag Glu	gat Asp	gtt Vai 70	aag Lys	cgt Arg	tta Leu	ggt Gly	gag Glu 75	aaa Lys	tat Tyr	tat Tyr	ctt Leu	atg Met 80	240
								tct Ser								288
gac Asp	tat Tyr	caa Gin	gaa Glu 100	aaa Lys	cat His	gaa Glu	gcc Ala	agt Ser 105	gaa Glu	ttt Phe	aaa Lys	gat Asp	ctc Leu 110	ttt Phe	tta Leu	336
aac Asn	tgg Trp	gat Asp 115	aag Lys	ttt Phe	tgg Trp	cca Pro	gaa Glu 120	aac Asn	cgt Arg	ccg Pro	aca Thr	cag Gln 125	tct Ser	gat Asp	gta Val	384
gat Asp	tta Leu 130	att Ile	tac Tyr	aag Lys	cgt Arg	aag Lys 135	gat Asp	cgt Arg	gca Ala	cca Pro	aag Lys 140	caa Gin	gag Glu	att He	gtt Val	432
ttt Phe 145	gaa Glu	gat Asp	ggg Gly	tca Ser	gtc Val 150	gaa Glu	cat His	t tg Leu	tgg Trp	aat Asn 155	acc Thr	ttt Phe	ggt Gly	gag Glu	gag Glu 160	480
cag Gln	att	gat Asp	ctt Leu	gat Asp 165	gtg Val	acc Thr	aaa Lys	gaa Glu	gta Val 170	act Thr	atg Met	gaa Glu	ttt Phe	atc 11e 175	cgt Arg	528
aag Lys	acc Thr	att	cag Gln 180	cac His	t t g Leu	gca Ala	agt Ser	aat Asn 185	ggg Gly	tgt Cys	gat Asp	t t g Leu	att lle 190	cgt Arg	cta Leu	576
gac Asp	gcc Ala	ttt Phe 195	gc t Ala	tat Tyr	gca Ala	gtg Val	aag Lys 200	aaa Lys	ttg Leu	gat Asp	act Thr	aat Asn 205	gat Asp	ttc Phe	ttt Phe	624
gta Val	gaa Glu 210	cca Pro	gat Asp	att lle	tgg Trp	gat Asp 215	t ta Leu	t t g Leu	gac Asp	aaa Lys	gtt Val 220	cga Arg	ga t Asp	atc	gc t Ala	672
						Leu		cct Pro							tcg Ser 240	720
att He	cag Gln	t t t Phe	aaa Lys	a t a e 245	Ala	gac Asp	cat His	gat Asp	tac Tyr 250	Туг	gtt Val	tat Tyr	ga t Asp	ttt Phe 255	Ala	768
c t t Leu	cca Pro	atg Met	gtg Val 260	Thr	c t t Leu	tat Tyr	act Thr	ctt Leu 265	tac Tyr	agt Ser	tcc Ser	aga Arg	aca Thr 270	Glu	cgt Arg	816
t t g Leu	gc t Ala	aag Lys 275	Trp	t t a Leu	aag Lys	atg Met	agc Ser 280	cca Pro	atg Met	aag Lys	caa Gin	ttt Phe 285	Thr	acg Thr	cta Leu	- 864
gac Asp	acc Thr 290	His	gat Asp	ggg Gly	at t	gga Gly 295	۷a۱	gtg Val	ga t Asp	gtc Val	aag Lys 300	ga t Asp	atc	t t g L e u	aca Thr	912
gat Asp 305	Glu	gag Glu	att	gac Asp	tat Tyr 310	Ala	tca Ser	aat Asn	gaa Glu	ctc Leu 315	Tyr	aag Lys	gtt Val	gga Gly	gct Ala 320	960
aat Asn	gtc Val	aaa Lys	cgt Arg	aag Lys 325	Tyr	t c c Se r	agt Ser	gcc Ala	gag Glu 330	Tyr	aa t Asn	aa t As n	tta Leu	gat Asp 335	He	1008

tac Tyr	caa Gin	atc Ile	aat Asn 340	tca Ser	acc Thr	tat Tyr	tat Tyr	tct Ser 345	gcg Ala	ctt Leu	gga Gly	gat Asp	gat Asp 350	gat Asp	gtc Val	1056
aag Lys	tat Tyr	ttc Phe 355	ctt Leu	gca Ala	cga Arg	tta Leu	att 11e 360	caa Gin	gca Ala	ttt Phe	gct Ala	cca Pro 365	ggt Gly	att	cct Pro	1104
caa GIn	gtt Val 370	tac Tyr	tat Tyr	gta Val	ggt Gly	cta Leu 375	tta Leu	gca Ala	ggc Gly	aag Lys	aat Asn 380	ga t Asp	ttg Leu	aaa Lys	tta Leu	1152
tta Leu 385	gaa Glu	gaa Glu	act Thr	aaa Lys	gta Val 390	gg t Gly	cga Arg	aat Asn	att ile	aat Asn 395	cgt Arg	cat His	tac Tyr	tat Tyr	agc Ser 400	1200
aat Asn	gag Glu	gaa Glu	ata Ile	gca Ala 405	gaa Glu	gaa Glu	gtc Val	caa Gin	cgt Arg 410	cct Pro	gta Val	gtg Val	aag Lys	gcc Ala 415	ctt Leu	1248
ctc Leu	aat Asn	cta Leu	ttt Phe 420	tct Ser	ttc Phe	cgt Arg	aat Asn	cga Arg 425	tca Ser	gta Val	gca Ala	ttt Phe	gat Asp 430	tta Leu	gaa Glu	1296
gga Gly	act Thr	att Ile 435	gac Asp	gtt Val	gaa Glu	aca Thr	cca Pro 440	aca Thr	gcc Ala	cac His	agc Ser	att He 445	gta Val	atc	aaa Lys	1344
cgt Arg	caa Gin 450	aat Asn	aaa Lys	gat Asp	aag Lys	tcc Ser 455	gta Val	aca Thr	gca Ala	gta Val	gca Ala 460	gaa Glu	att	gat Asp	ttg Leu	1392
caa Gin 465	aat Asn	cag Gin	act Thr	tat Tyr	cga Arg 470	gta Val	atg Met	aga Arg	acg Thr	gaa Glu 475	tgg Trp	aag Lys	tac Tyr	att Ile	ttg Leu 480	1440
	act Thr															1446
<21 <21		12 482														

<211> 402
<212> PRT
<213> Streptococcus mitis

Met Pro IIe Gin Asn Lys Thr Met Leu IIe Thr Tyr Ser Asp Ser Leu 1 10 15

Gly Asn Asn Leu Lys Asp Leu Tyr Glu Asn Leu Glu Glu Tyr Phe Gly $20 \hspace{1cm} 25 \hspace{1cm} 30$

Asp Ala lie Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly 35 40 45

Asp Arg Gly Phe Ala Pro Val Asp Tyr Asp Glu Val Asp Ser Ala Phe $50\,$

Gly Asp Trp Glu Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met 65 70 75 80

Phe Asp Phe Met IIe Asn His IIe Ser Arg Gln Ser Lys Tyr Tyr Lys 85 90 95

Asp Tyr Gin Glu Lys His Glu Ala Ser Glu Phe Lys Asp Leu Phe Leu 100 105 110

Asn Trp Asp Lys Phe Trp Pro Glu Asn Arg Pro Thr Gln Ser Asp Val 115 120 125

Asp Leu lie Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gin Giu lie Val 130 135 140

EG014US-Sequence Listing.txt Page 19

Phe Glu Asp Gly Ser Val Glu His Leu Trp Asn Thr Phe Gly Glu Glu 145 150 155 160

Gin lie Asp Leu Asp Val Thr Lys Giu Val Thr Met Giu Phe lie Arg 165 170 175

Lys Thr lle Gln His Leu Ala Ser Asn Gly Cys Asp Leu lle Arg Leu 180 185 190

Asp Ala Phe Ala Tyr Ala Val Lys Leu Asp Thr Asn Asp Phe Phe 195 200 205

Val Glu Pro Asp lle Trp Asp Leu Leu Asp Lys Val Arg Asp lle Ala 210 215 220

Ala Glu Tyr Gly Thr Glu Leu Leu Pro Glu lle His Glu His Tyr Ser 225 230 235 240

lie Gin Phe Lys lie Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala 245 250 255

Leu Pro Met Val Thr Leu Tyr Thr Leu Tyr Ser Ser Arg Thr Glu Arg 260 270

Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gin Phe Thr Thr Leu 275 280 285

Asp Thr His Asp Gly IIe Gly Val Val Asp Val Lys Asp IIe Leu Thr 290 295 300

Asp Glu Glu lle Asp Tyr Ala Ser Asn Glu Leu Tyr Lys Val Gly Ala 305 310 315 320

Asn Val Lys Arg Lys Tyr Ser Ser Ala Glu Tyr Asn Asn Leu Asp lie 325 330 335

Tyr Gin ile Asn Ser Thr Tyr Tyr Ser Aia Leu Giy Asp Asp Asp Val

Lys Tyr Phe Leu Ala Arg Leu Ile Gin Ala Phe Ala Pro Gly Ile Pro 355 360 365

Gin Vai Tyr Tyr Vai Giy Leu Leu Aia Giy Lys Asn Asp Leu Lys Leu 370 375 380

Leu Glu Glu Thr Lys Vai Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser 385 390 395 400

Asn Giu Giu ile Ala Giu Giu Val Gin Arg Pro Val Val Lys Ala Leu 405 410 415

Leu Asn Leu Phe Ser Phe Arg Asn Arg Ser Val Ala Phe Asp Leu Glu 420 430

Gly Thr lle Asp Val Glu Thr Pro Thr Ala His Ser Ile Val Ile Lys 435 440 445

Arg Gin Asn Lys Asp Lys Ser Val Thr Ala Val Ala Giu lle Asp Leu 450 455 460

Gin Asn Gin Thr Tyr Arg Val Met Arg Thr Giu Trp Lys Tyr Ile Leu 465. 470 475 480

<210 <211 <212 <213	>	13 1458 DNA Leuco	nost	ос п	iesen	itero	ides	ì								
<220 <221 <222	>	CDS (1)	(145	i8)												
<400 atg Met 1	gaa	13 att lle	caa GIn	aac Asn 5	aaa Lys	gca Ala	atg Met	ctc Leu	att lie 10	acg Thr	tat Tyr	gct Ala	gat Asp	tct Ser 15	t tg Leu	48
ggc Gly	agt Ser	aa t As n	atc Ile 20	aag Lys	gaa Glu	gtc Val	cac His	caa Gin 25	gtt Val	t t g Leu	aag Lys	gaa Glu	gac Asp 30	att Ile	ggc Gly	96
gat Asp	gcg Ala	att lle 35	ggc Gly	ggg G1y	gta Val	cat His	ttg Leu 40	t t a Leu	cca Pro	ttt Phe	ttc Phe	cct Pro 45	tct Ser	aca Thr	ggt Giy	144
gat Asp	cgt Arg 50	ggc Gly	ttc Phe	gcc Ala	cct Pro	tct Ser 55	gat Asp	tac Tyr	acg Thr	cgt Arg	gtt Val 60	gat Asp	gca Ala	aca Thr	ttt Phe	192
ggt Gly 65	gat Asp	tgg Trp	aat Asn	gat Asp	gtt Val 70	gag Glu	gca Ala	ctt Leu	ggg Gly	caa Gin 75	gaa Glu	tac Tyr	tat Tyr	ttg Leu	atg Met 80	240
ttt Phe	ga t Asp	ttt Phe	atg Met	atc lle 85	aat Asn	cat His	att Ile	tct Ser	cgt Arg 90	gaa Glu	tcg Ser	gag Glu	atg Met	tat Tyr 95	caa Gin	288
		aaa Lys														336
cgc Arg	tgg Trp	gaa Glu 115	aag Lys	ttt Phe	tgg Trp	caa Gln	cag Gln 120	gc t Ala	ggg Gly	cca Pro	gat Asp	cga Arg 125	cca Pro	act Thr	caa Gin	384
gca Ala	gac Asp 130	gtc Val	gac Asp	ctt Leu	att He	tat Tyr 135	aag Lys	cgc Arg	aaa Lys	gac Asp	aag Lys 140	gcg Ala	cca Pro	att He	caa GIn	432
gaa Glu 145	ato	act Thr	ttt Phe	gct Ala	gac Asp 150	ggt Gly	acg Thr	aca Thr	gag Glu	cat His 155	ctt Leu	tgg Trp	aat Asn	aca Thr	ttt Phe 160	480
ggt Gly	gaa Glu	gaa Glu	caa Gln	att 11e 165	gat Asp	att lle	gat Asp	gtt Val	aat Asn 170	tct Ser	caa Gin	att	gc t Ala	aaa Lys 175	gcc Ala	528
ttc Phe	ati He	aaa Lys	gca Ala 180	acg Thr	cta Leu	gaa Glu	gac Asp	atg Met 185	gtc Val	caa Gln	cat His	ggt Gly	gcc Ala 190	aat Asn	t t g Leu	576
att Ile	cgt Arg	t tta g Leu 195	gat Asp	gct Ala	ttc Phe	gcc Ala	tat Tyr 200	gct Ala	gtt Val	aag Lys	aaa Lys	gtt Val 205	ggg Gly	aca Thr	aat Asn	624
gat Asp	t t d Phe 210	ttt Phe	gtc Val	gaa Glu	cca Pro	gaa Glu 215	ata Ile	tgg Trp	act Thr	gtt Val	tta Leu 220	aac Asn	gaa Glu	gtg Val	cgt Arg	672
gac Asp 225	ati	t ttg E Leu	gca Ala	cct Pro	atg Met 230	cat His	gct Ala	gaa Glu	att	tta Leu 235	cca Pro	gaa Giu	att Ile	cat His	gag Glu 240	720
cat His	ta: Ty:	t aca r Thr	att	cct Pro 245	caa Gln	aag Lys	atc	aac Asn	gcc Ala 250	cat His	ggt Gly	tat Tyr	ttc Phe	act Thr 255	tat Tyr	768
ga t Asp	t t t	t gct e Ala	ttg Leu 260	cca Pro	atg Met	aca Thr	gta Val	ctt Leu 265	tat Tyr	acg Thr	ctt Leu	tac Tyr	tca Ser 270	ggc Gly	aaa Lys	816
aca Thr	aa† Ası	t cga n Arg 275	c ta Leu	gcc Ala	aac Asn	tgg Trp	ctc Leu 280	aaa Lys	cag Gin	tct Ser	ccg Pro	atg Met 285	aaa Lys	caa Gin	ttc Phe	864

acg Thr	acg Thr 290	tta Leu	ga t Asp	acg Thr	cat His	gat Asp 295	ggc Gly	att He	GIY	gtt Val	gtt Val 300	gac Asp	gca Ala	cgt Arg	gat. Asp	912
att ile 305	t t g Leu	aca Thr	gac Asp	gaa Glu	gaa Glu 310	att ile	gat Asp	tat Tyr	gct Ala	tct Ser 315	gag Glu	gaa Glu	tta Leu	tac Tyr	aaa Lys 320	960
gtt Val	gga Gly	gcc Ala	aa t As n	gtc Val 325	aaa Lys	aag Lys	acc Thr	tac Tyr	tca Ser 330	tca Ser	gc t Ala	gcg Ala	tat Tyr	aat Asn 335	aac Asn	1008
tta Leu	gat Asp	att ile	tat Tyr 340	cag Gln	att Ile	aa t As n	tca Ser	act Thr 345	tac Tyr	tat Tyr	tca Ser	gc t Ala	tta Leu 350	ggc Gly	aat Asn	1056
gat Asp	gat Asp	gcc Ala 355	gca Ala	tat Tyr	ttg Leu	ttg Leu	agt Ser 360	cgt Arg	gtt Val	ttc Phe	caa Gin	gtc Val 365	ttt Phe	gca Ala	cct Pro	1104
ggt Gly	att 11e 370	cca Pro	caa Gln	att	tat Tyr	tat Tyr 375	gtc Val	ggg Gly	t t a Leu	c t t Leu	gca Ala 380	ggt Gly	gag Glu	aat Asn	ga t Asp	1152
att lle 385	gat Asp	t t g Leu	ttg Leu	gaa Glu	tct Ser 390	tca Ser	aaa Lys	gaa Glu	ggt Gly	cgt Arg 395	aat Asn	att	aat Asn	cgt Arg	cat His 400	1200
tac Tyr	tat Tyr	act Thr	cgt Arg	gaa Glu 405	gaa Glu	ata ile	aaa Lys	tca Ser	gct Ala 410	gtt Val	aag Lys	cgg Arg	cca Pro	gtt Val 415	gtt Val	1248
gct Ala	gac Asp	tta Leu	ttg Leu 420	gca Ala	tta Leu	tta Leu	tca Ser	tgg Trp 425	cgt Arg	aat Asn	cag Gin	ttt Phe	tca Ser 430	gca Ala	ttt Phe	1296
gct Ala	ctg Leu	gat Asp 435	ggg Gly	aca Thr	atc	ac t Thr	gtc Val 440	gag Glu	aca Thr	cca Pro	tca Ser	gaa Glu 445	cat His	gat Asp	att	1344
aaa Lys	att IIe 450	aca Thr	cga Arg	acg Thr	gat Asp	cat His 455	tcc Ser	gga Gly	gat Asp	aat Asn	ata Ile 460	gct Ala	att	t tg Leu	cta Leu	1392
gct Ala 465	aa t As n	gcc Ala	aag Lys	aca Thr	cgc Arg 470	acc Thr	ttt Phe	gtc Val	atc Ile	aca Thr 475	gca Ala	aat Asn	ggc Gly	aag Lys	aca Thr 480	1440
		caa Gin		aaa Lys 485	taa											1458

<210> 14
<211> 485
<212> PRT
<213> Leuconostoc mesenteroides

Met Glu lle Gln Asn Lys Ala Met Leu lle Thr Tyr Ala Asp Ser Leu 1 10 15

Gly Ser Asn Ile Lys Glu Val His Gln Val Leu Lys Glu Asp Ile Gly 20 25 30

Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly 35 40 45

Asp Arg Gly Phe Ala Pro Ser Asp Tyr Thr Arg Val Asp Ala Thr Phe 50 60

Gly Asp Trp Asn Asp Val Glu Ala Leu Gly Gln Glu Tyr Tyr Leu Met 65 70 75

Phe Asp Phe Met 11e Asn His 11e Ser Arg Glu Ser Glu Met Tyr Gln. $85\,$ $90\,^{\circ}$

EG014US-Sequence Listing.txt Page 2

Asp Phe Lys Ala Asn His Asp Gln Ser Lys Tyr Arg Asp Phe Phe Ile 100 105 110

Arg Trp Glu Lys Phe Trp Gln Gln Ala Gly Pro Asp Arg Pro Thr Gln 115 120 125

Ala Asp Val Asp Leu Ile Tyr Lys Arg Lys Asp Lys Ala Pro Ile Gin 130 135 140

Glu lle Thr Phe Ala Asp Gly Thr Thr Glu His Leu Trp Asn Thr Phe 145 150 155 160

Gly Glu Glu Gln lle Asp lle Asp Val Asn Ser Gln lle Ala Lys Ala 165 170 175

Phe IIe Lys Ala Thr Leu Glu Asp Met Val Gln His Gly Ala Asn Leu 180 185 190

lle Arg Leu Asp Ala Phe Ala Tyr Ala Val Lys Lys Val Gly Thr Asn 195 200 205

Asp Phe Phe Val Glu Pro Glu lie Trp Thr Val Leu Asn Glu Val Arg 210 215 ... 220

Asp Ile Leu Ala Pro Met His Ala Glu Ile Leu Pro Glu Ile His Glu 225 230 235 240

His Tyr Thr lle Pro Gln Lys lle Asn Ala His Gly Tyr Phe Thr Tyr 245 250 255

Asp Phe Ala Leu Pro Met Thr Val Leu Tyr Thr Leu Tyr Ser Gly Lys 260 270

Thr Asn Arg Leu Ala Asn Trp Leu Lys Gin Ser Pro Met Lys Gin Phe 275 280 285

Thr Thr Leu Asp Thr His Asp Gly 11e Gly Val Val Asp Ala Arg Asp 290 . 295 300

ile Leu Thr Asp Glu Glu ile Asp Tyr Ala Ser Glu Glu Leu Tyr Lys 305 310 315

Val Giy Ala Asn Val Lys Lys Thr Tyr Ser Ser Ala Ala Tyr Asn Asn 325 330 335

Leu Asp ile Tyr Gin ile Asn Ser Thr Tyr Tyr Ser Ala Leu Giy Asn $340 \hspace{1.5cm} 345 \hspace{1.5cm} 350 \hspace{1.5cm}$

Asp Asp Ala Ala Tyr Leu Leu Ser Arg Val Phe Gln Val Phe Ala Pro 355 360 365

Gly lie Pro Gin lie Tyr Tyr Val Gly Leu Leu Ala Gly Glu Asn Asp 370 375 380

lle Asp Leu Leu Glu Ser Ser Lys Glu Gly Arg Asn lle Asn Arg His 385 390 395 400

Tyr Tyr Thr Arg Glu Glu Ite Lys Ser Ala Val Lys Arg Pro Val Val 405. 410 415

Ala Asp Leu Leu Ala Leu Leu Ser Trp Arg Asn Gin Phe Ser Ala Phe 420 425 430

Ala Leu Asp Gly Thr lle Thr Val Glu Thr Pro Ser Glu His Asp lle

440

445

Lys lie Thr Arg Thr Asp His Ser Gly Asp Asn lie Ala lie Leu Leu 450 460

Ala Asn Ala Lys Thr Arg Thr Phe Val lle Thr Ala Asn Gly Lys Thr 465 470 475 480

Val Leu Gin Asn Lys 485

<210> 15 <211> 1443 <212> DNA

<212> DNA <213> Lactobacillus acidophilus

<220> <221> CDS <222> (1)..(1443)

<400> 15
atg aaa tta caa aat aag gca ata ttg ata act tat cca gat agt tta
48
Met Lys Leu Gln Asn Lys Ala IIe Leu IIe Thr Tyr Pro Asp Ser Leu
1
1
10
15

ggt cat aat ttg aag gac ttg gat cat gta atg gat cgc tat ttt aat Gly His Asn Leu Lys Asp Leu Asp His Val Met Asp Arg Tyr Phe Asn 20 25 30

aaa acg ata ggt ggt att cat tta tta cca ttt ttc cct tca aac ggt Lys Thr lie Gly Gly lie His Leu Leu Pro Phe Phe Pro Ser Asn Gly 35 40 45

gat cgc ggt ttt tct cct aca aga tat gat gta gtt gag cct aag ttt
Asp Arg Gly Phe Ser Pro Thr Arg Tyr Asp Val Val Glu Pro Lys Phe
50 60

ggt tca tgg gaa gat gta gaa aag tta agt caa aag tat tat ttg atg
Gly Ser Trp Glu Asp Val Glu Lys Leu Ser Gln Lys Tyr Tyr Leu Met
65 70 80

ttt gac ttt atg att aat cat ctt tct aaa aaa tcc tca tat ttt gaa 288 Phe Asp Phe Met Ile Asn His Leu Ser Lys Lys Ser Ser Tyr Phe Glu 85 90 95

gat tit gaa gcc aag cac gat aaa agc aaa tat agc gat cit tic tia Asp Phe Glu Ala Lys His Asp Lys Ser Lys Tyr Ser Asp Leu Phe Leu 100 105 110

agt tgg gat aaa ttt tgg cca aag ggc aga cca act aaa gaa gat ata
Ser Trp Asp Lys Phe Trp Pro Lys Giy Arg Pro Thr Lys Giu Asp lie
115 120 125

gat tta att tat aaa cga aaa gat aag gcc cca tat caa aat att aaa Asp Leu lle Tyr Lys Arg Lys Asp Lys Ala Pro Tyr Gin Asn lle Lys 130 140

ttt gaa gat ggt act cat gaa aag atg tgg aat act ttc ggc cca gat
Phe Glu Asp Gly Thr His Glu Lys Met Trp Asn Thr Phe Gly Pro Asp
145
150
160

caa atg gat ttg gat gtt aga acc aag aca aca caa gat ttt ata aag
Gin Met Asp Leu Asp Val Arg Thr Lys Thr Thr Gin Asp Phe lie Lys
165 170 175

cat aat tta caa aat ctt tct aaa cat ggt gct agt ttg att cgt tta
His Asn Leu Gin Asn Leu Ser Lys His Gly Ala Ser Leu Ile Arg Leu
180 185 190

gat gca ttt gct tat gca att aaa aag tta gat aca aat gac ttc ttt
Asp Ala Phe Ala Tyr Ala ile Lys Leu Asp Thr Asn Asp Phe Phe
195 200 205

gta gaa ccg gaa att tgg aat tta ctc gaa aag gta aat gat tat ctt Val Glu Pro Glu lie Trp Asn Leu Leu Glu Lys Val Asn Asp Tyr Leu 210 215 220

asa gat act cca act act att ctg cct gas att cat gag cat tat acg
Lys Asp Thr Pro Thr Thr Ile Leu Pro Glu Ile His Glu His Tyr Thr
225 230 235 240

atg Met	cca Pro	ttt Phe	aag Lys	gtg Val 245	gca Ala	gaa Glu	cat His	gga Gly	tac Tyr 250	t t t Phe	att	tat Tyr	ga t Asp	ttt Phe 255	gc t A I a	768
tta Leu	cca Pro	atg Met	gta Va! 260	ttg Leu	ttg Leu	tat Tyr	tca Ser	ctt Leu 265	tat Tyr	agc Ser	ggt Gly	aa t As n	agt Ser 270	act Thr	caa Gin	816
ctt Leu	gct Ala	gct Ala 275	tgg Trp	cta Leu	aag Lys	aaa Lys	tgt Cys 280	ccg Pro	atg Met	aag Lys	caa GIn	ttt Phe 285	act Thr	ac t Thr	tta Leu	864
gat Asp	acc Thr 290	cac His	gat Asp	gga Gly	tta Leu	ggc Gly 295	gta Val	gtt Val	gac Asp	gca) Ala	aag Lys 300	gat Asp	att	ctt Leu	acg Thr	912
gac Asp 305	gat Asp	caa Gin	att ile	agc Ser	tac Tyr 310	aca Thr	aca Thr	aac Asn	gaa Glu	ctt Leu 315	tat Tyr	aaa Lys	att	ggt Gly	gct Ala 320	960
aac Asn	gtc Val	aag Lys	aag Lys	aaa Lys 325	tat Tyr	tct Ser	agt Ser	gct Ala	gaa Glu 330	tat Tyr	cat His	aat Asn	ttg Leu	gat Asp 335	att Ile	1008
tat Tyr	caa Gin	att	aat Asn 340	act Thr	act Thr	tat Tyr	tat Tyr	tct Ser 345	gca Ala	t t g Leu	ggt Gly	aat Asn	gat Asp 350	gat Asp	aaa Lys	1056
aaa Lys	tat Tyr	ttt Phe 355	att ile	gca Ala	cgg Arg	tta Leu	tta Leu 360	caa Gln	atc Ile	ttt Phe	gcc Ala	cct Pro 365	ggt Gly	att	cca Pro	1104
caa Gin	att lle 370	tat Tyr	tat Tyr	gtt Val	gga Gly	ttg Leu 375	tta Leu	gca Ala	gga Gly	gaa Glu	aat Asn 380	gat Asp	att He	caa Gin	tta Leu	1152
	Ğlü			aaa Lys												1200
t t g Leu	gat Asp	gag Glu	att He	gcg Ala 405	gaa Glu	caa Gln	gtt Val	caa Gin	aga Arg 410	cct Pro	gta Val	gta Val	aaa Lys	tct Ser 415	ttg Leu	1248
att He	aag Lys	tta Leu	ttg Leu 420	gaa Glu	ttt Phe	cgt Arg	aat Asn	tct Ser 425	gta Val	cct Pro	gca Ala	ttt Phe	gat Asp 430	ttg Leu	gaa Glu	1296
gg t Gly	tca Ser	atc lle 435	Lys	gtt Val	gaa Glu	act Thr	cca Pro 440	agt Ser	gaa Glu	cat His	gaa Glu	att Ile 445	att Ile	gtc Val	act Thr	1344
aga Arg	tca Ser 450	Asn	aag Lys	gca Ala	gga Gly	aca Thr 455	Glu	gta Val	gct Ala	agt Ser	acg Thr 460	tac Tyr	gta Val	gac Asp	ttt Phe	1392
aag Lys 465	Asn	t t a Leu	gac Asp	tat Tyr	caa Gin 470	Val	aaa Lys	tac Tyr	aat Asn	gat Asp 475	cag Gin	gtc Val	ttt Phe	aa t Asn	ttt Phe 480	1440
tag	:															1443
/21	۵\	16														
<21 <21	1>	16 480 DDT														
<21 <21	3>	PRT Lact	obac	illu	s ac	i dop	hilu	s								
<40	0>	16														

Met Lys Leu Gin Asn Lys Ala lie Leu lie Thr Tyr Pro Asp Ser Leu 1 5 10 15

Gly His Asn Leu Lys Asp Leu Asp His Val Met Asp Arg Tyr Phe Asn 20 25

Lys Thr lie Gly Gly lie His Leu Leu Pro Phe Phe Pro Ser Asn Gly 35 40 45

Asp Arg Gly Phe Ser Pro Thr Arg Tyr Asp Val Val Glu Pro Lys Phe 50 55 60

Gly Ser Trp Glu Asp Val Glu Lys Leu Ser Gln Lys Tyr Tyr Leu Met 65 70 75 80 Phe Asp Phe Met IIe Asn His Leu Ser Lys Lys Ser Ser Tyr Phe Glu 85 90 95 Asp Phe Glu Ala Lys His Asp Lys Ser Lys Tyr Ser Asp Leu Phe Leu 100 105 110 Ser Trp Asp Lys Phe Trp Pro Lys Gly Arg Pro Thr Lys Glu Asp Ile Asp Leu lie Tyr Lys Arg Lys Asp Lys Ala Pro Tyr Gin Asn lie Lys 130 135 140 Phe Glu Asp Gly Thr His Glu Lys Met Trp Asn Thr Phe Gly Pro Asp 145 150 160 Gin Met Asp Leu Asp Val Arg Thr Lys Thr Thr Gin Asp Phe lie Lys 165 170 175 His Asn Leu Gin Asn Leu Ser Lys His Gly Ala Ser Leu Ile Arg Leu 180 185 190 Asp Ala Phe Ala Tyr Ala IIe Lys Lys Leu Asp Thr Asn Asp Phe Phe 195 200 205 Val Glu Pro Glu 11e Trp Asn Leu Leu Glu Lys Val Asn Asp Tyr Leu 210 215 220 Lys Asp Thr Pro Thr Thr IIe Leu Pro Glu IIe His Glu His Tyr Thr 225 230 235 240 Met Pro Phe Lys Val Ala Glu His Gly Tyr Phe lle Tyr Asp Phe Ala 245 250 255 Leu Pro Met Val Leu Leu Tyr Ser Leu Tyr Ser Gly Asn Ser Thr Gln 260 265 270 Leu Ala Ala Trp Leu Lys Lys Cys Pro Met Lys Gln Phe Thr Thr Leu 275 280 285 Asp Thr His Asp Gly Leu Gly Val Val Asp Ala Lys Asp Ile Leu Thr 290 295 300 Asp Asp Gin lie Ser Tyr Thr Thr Asn Giu Leu Tyr Lys lie Gly Ala 305 310 315 320 Asn Val Lys Lys Tyr Ser Ser Ala Glu Tyr His Asn Leu Asp Ile 325 330 335 Tyr Gin ile Asn Thr Thr Tyr Tyr Ser Ala Leu Gly Asn Asp Asp Lys 340 345 350 Lys Tyr Phe Ile Ala Arg Leu Leu Gin Ile Phe Ala Pro Giy Ile Pro 355 360 365 Gin lie Tyr Tyr Val Giy Leu Leu Ala Giy Giu Asn Asp lie Gin Leu 370 375 380 Leu Glu Lys Thr Lys Glu Gly Arg Asp Ile Asn Arg His Tyr Tyr Asp 385 390 395

Leu Asp Glu lle Ala Glu Gln Val Gln Arg Pro Val Val Lys Ser Leu 405 410 415 lle Lys Leu Leu Glu Phe Arg Asn Ser Val Pro Ala Phe Asp Leu Glu 420 425 430 Gly Ser lle Lys Val Glu Thr Pro Ser Glu His Glu IIe IIe Val Thr 435 440 445 Arg Ser Asn Lys Ala Gly Thr Glu Val Ala Ser Thr Tyr Val Asp Phe 450 455 460 Lys Asn Leu Asp Tyr Gin Vai Lys Tyr Asn Asp Gin Vai Phe Asn Phe 465 470 475 <210> 17
<211> 1443
<212> DNA
<213> Lacto Lactobacillus acidophilus <220> <221> CDS <222> (1)..(1443) **<400> 17** atg cca att gaa aat aaa gta atg tta att act tat cca gac agt ttg Met Pro lie Glu Asn Lys Val Met Leu lie Thr Tyr Pro Asp Ser Leu 1 10 15 96 ggt aaa aat tta aaa gaa tta gat gaa att tta agt gaa gac ttg aag Gly Lys Asn Leu Lys Glu Leu Asp Glu IIe Leu Ser Glu Asp Leu Lys 20 25 30 ggg gct gta ggc ggt att cac tta ttg cca ttc ttc cca tca act ggt Gly Ala Val Gly Gly Ile His Leu Leu Pro Phe Phe Pro Ser Thr Gly 35 40 45 144 gac cgt gga ttt gct ccg act gga tat aca gaa gta gat cct aag ttt Asp Arg Gly Phe Ala Pro Thr Gly Tyr Thr Glu Val Asp Pro Lys Phe 50 55 60 ggt gat tgg tca gac att gaa aaa ata ggt aag aaa tat tat ttg atg Gly Asp Trp Ser Asp lie Glu Lys lie Gly Lys Lys Tyr Tyr Leu Met 65 70 75 80 240 288 ttt gat ttt atg att aat cat att tct cgt caa tca aaa ttt tat aaa Phe Asp Phe Met IIe Asn His IIe Ser Arg Gln Ser Lys Phe Tyr Lys 85 90 95 gat ttc aaa caa aag aaa gat aaa agt aag tat gcc gat tta ttt ttg Asp Phe Lys Gln Lys Lys Asp Lys Ser Lys Tyr Ala Asp Leu Phe Leu 100 105 110 336 agc tgg gac aaa ttt tgg ccg gaa ggt cgt cca act cga aaa gat att Ser Trp Asp Lys Phe Trp Pro Glu Gly Arg Pro Thr Arg Lys Asp Ile 115 120 125 gat tta att tat aaa cga aaa gat cgt gct cca tat caa gaa att act Asp Leu lie Tyr Lys Arg Lys Asp Arg Ala Pro Tyr Gin Glu lie Thr 130 135 140 432 ttt aca gat ggc agt aaa gaa aaa tta tgg aat act ttt ggt gaa gag Phe Thr Asp Gly Ser Lys Glu Lys Leu Trp Asn Thr Phe Gly Glu Glu 145 150 160 480 528 caa atc gat atg gat gtt cga aag gag gtg aca cag aag ttt att aaa Gin ile Asp Met Asp Val Arg Lys Giu Val Thr Gin Lys Phe Ile Lys 165 170 175 gat acg ttg aga gca tta att gat cat ggt gct gat att att cgg tta Asp Thr Leu Arg Ala Leu lle Asp His Gly Ala Asp lle lle Arg Leu 180 185 190 576 gat gct ttt gcg tat gct gta aag aag tta gat act aat gat ttc ttt Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe 195 200 205 624 672

gta gag cca gaa att tgg gat tta cta aaa caa gta caa gat gat att

EG014US-Sequence Li	sting.txt	Page 27	
Val Glu Pro Glu lle 210	Trp Asp Leu 215	Leu Lys Gin Val Gin Asp Asp 220	lle
		cca gaa ata cat gaa cac tat Pro Glu IIe His Glu His Tyr 235	
		gga tat tat atc tat gac ttt Gly Tyr Tyr lle Tyr Asp Phe 250 255	
		ctt tat tca ggt aag tcc aat Leu Tyr Ser Gly Lys Ser Asn 265 270	
		cca atg aaa cag ttc act acc Pro Met Lys Gln Phe Thr Thr 285	
gat aca cat gat ggt Asp Thr His Asp Gly 290	atc ggt gtt ile Gly Val 295	gtt gat gct cgt gat att ctc Val Asp Ala Arg Asp lie Leu 300	tcc 912 Ser
cct gac gaa att aaa Pro Asp Glu lle Lys 305	tac aca agt Tyr Thr Ser 310	aat gaa ttg tat aaa gtt gga Asn Glu Leu Tyr Lys Val Gly 315	gct 960 Ala 320
		gcc gaa tat cat aat tta gat Ala Glu Tyr His Asn Leu Asp 330 335	
		tct gct tta ggc aat gat gat Ser Ala Leu Gly Asn Asp Asp 345 350	
		caa atg ttt gcg cct ggt att Gin Met Phe Ala Pro Gly Ile 365	
		gct ggt aaa aac gat atc gaa Ala Gly Lys Asn Asp lle Glu 380	
		aac att aat cgt cat tac tat : Asn lle Asn Arg His Tyr Tyr : 395	
		aaa aga cct tta gta gca gca Lys Arg Pro Leu Val Ala Ala 410 415	
		aat gaa gca gct ttt gat ctt Asn Glu Ala Ala Phe Asp Leu 425 430	
gga tcc att gaa atc Gly Ser lle Glu lle 435	act acg cct Thr Thr Pro 440	aat gaa aac gtg att caa ata Asn Glu Asn Val Ile Gin Ile 445	act 1344 Thr
		aaa gca aga gct gtt att aat Lys Ala Arg Ala Val Ile Asn (460	
aaa aat tta act tat Lys Asn Leu Thr Tyr 465	caa gtg act Gin Val Thr 470	gta aat aat gag gtt att aac Val Asn Asn Glu Val Ile Asn I 475	ttt 1440 Phe 480
taa			1443
<pre><210> 18 <211> 480 <212> PRT <213> Lactobacillus</pre>	s acidophilus		
<400> 18			
Met Pro IIe Glu Asn 1 5	Lys Val Met	Leu lle Thr Tyr Pro Asp Ser I 10 15	Leu

Gly Lys Asn Leu Lys Glu Leu Asp Glu lle Leu Ser Glu Asp Leu Lys 25 30

EG014US-Sequence Listing.txt Page 28

Gly Ala Val Gly Gly 11e His Leu Leu Pro Phe Phe Pro Ser Thr Gly $35^{\rm .}$

Asp Arg Gly Phe Ala Pro Thr Gly Tyr Thr Glu Val Asp Pro Lys Phe 50 55 60

Gly Asp Trp Ser Asp Ile Glu Lys Ile Gly Lys Lys Tyr Tyr Leu Met 65 70 75 80

Phe Asp Phe Met IIe Asn His IIe Ser Arg Gln Ser Lys Phe Tyr Lys 85 90 95

Asp Phe Lys Gin Lys Lys Asp Lys Ser Lys Tyr Ala Asp Leu Phe Leu 100 105 110

Ser Trp Asp Lys Phe Trp Pro Glu Gly Arg Pro Thr Arg Lys Asp Ile 115 120 125

Asp Leu lle Tyr Lys Arg Lys Asp Arg Ala Pro Tyr Gln Glu lle Thr 130 135 140

Phe Thr Asp Gly Ser Lys Glu Lys Leu Trp Asn Thr Phe Gly Glu Glu 145 150 155 160

Gin lie Asp Met Asp Vai Arg Lys Giu Vai Thr Gin Lys Phe lie Lys 165 170 175

Asp Thr Leu Arg Ala Leu IIe Asp His Gly Ala Asp IIe IIe Arg Leu 180 185 190

Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe 195 200 205

Val Glu Pro Glu IIe Trp Asp Leu Leu Lys Gln Val Gln Asp Asp IIe 210 215 220

Ser Asp Lys Gly Ala Met 11e Leu Pro Glu IIe His Glu His Tyr Ser 225 230 235 240

Met Pro Phe Lys Ile Ser Lys His Gly Tyr Tyr Ile Tyr Asp Phe Ala 245 250 255

Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Ser Asn Arg 260 265 270

Leu Ala Asp Trp Leu Lys Lys Cys Pro Met Lys Gln Phe Thr Thr Leu 275 280 285

Asp Thr His Asp Gly Ile Gly Val Val Asp Ala Arg Asp Ile Leu Ser 290 295 300

Pro Asp Giu ile Lys Tyr Thr Ser Asn Giu Leu Tyr Lys Val Giy Ala 305 310 315 320

Asn Val Lys Lys Tyr Ser Ser Ala Glu Tyr His Asn Leu Asp lle 325 330 335

Tyr Gin ile Asn Thr Thr Tyr Tyr Ser Ala Leu Gly Asn Asp Asp Lys 340 345 350

Lys Tyr Phe lie Ala Arg Leu lie Gin Met Phe Ala Pro Gly lie Pro-355 360 365

Gin Val Tyr Tyr Val Gly Met Leu Ala Gly Lys Asn Asp lie Glu Leu

370	375		380	
Leu Glu Lys Thr 385	Lys Glu Gly A 390	rg Asn lie Asn 395	Arg His Tyr Tyr	Gly 400
Arg Glu Glu Val	Ala Glu Glu Ti 405	hr Lys Arg Pro 410	Leu Val Ala Ala 415	Leu
Leu Lys Leu Phe 420	Asn Phe Arg As	sn Asn Glu Ala 425	Ala Phe Asp Leu 430	Asp
Gly Ser lle Glu 435		ro Asn Glu Asn 40	Vai lie Gin lie 445	Thr
Arg Met Asn Lys 450	Asp Lys Thr A 455	rg Lys Ala Arg	Ala Val ile Asn 460	Leu
Lys Asn Leu Thr 465	Tyr Gin Val Ti 470	hr Val Asn Asn 475	Glu Val lle Asn	Phe 480
<pre><210> 19 <211> 1443 <212> DNA <213> Listeria</pre>	monocytogenes			
<220> <221> CDS <222> (1)(144	43)			
<400> 19 atg caa att aaa Met Gin lie Lys 1	aat aaa gct a Asn Lys Ala M 5	tg tta att act et Leu Ile Thr 10	tat tot gat agt Tyr Ser Asp Ser 15	tta 48 Leu
			gaa act tat ttt Glu Thr Tyr Phe 30	
		eu Leu Pro Phe	ttt cca tcc act Phe Pro Ser Thr 45	
			gta gat agc gac Val Asp Ser Asp 60	
Gly Ser Trp Glu 65	lie lie Glu Ly 70	ys Leu Gly Glu 75	aag tat tat tta Lys Tyr Tyr Leu	Met 80
ttt gat ttt atg Phe Asp Phe Met	att aat cac a lle Asn His l 85	tt tct cgc gaa le Ser Arg Glu 90	tca ctc ttc ttt Ser Leu Phe Phe 95	Gin
			aaa gat atg ttt Lys Asp Met Phe 110	lle
	Phe Phe Pro P		aat gaa aaa gac Asn Glu Lys Asp 125	Leu
			ttt caa gaa gtt Phe Gin Giu Val 140	Glu
Phe Ala Asp Gly 145.	Gly Thr Glu Lo 150:	eu Val Trp Asn 155	act ttt ggg gaa Thr Phe Gly Glu	Glu 160
Gin ile Asp Leu	Asp Val Thr A 165	la Ğlu Val Thr 170:	aaa gaa ttt att Lys Glu Phe lie 175	Arg
			tct att ttg cgt Ser lle Leu Arg 190	

													aat Asn 205				624
													aaa Lys				672
,													gaa Glu				720
													tat Tyr				768
													cga Arg				816
													ttt Phe 285				864
1	gat Asp	acg Thr 290	cat His	gat Asp	ggc Gly	att He	ggc Gly 295	gtt Vai	gtg Val	gat Asp	gca Ala	cgc Arg 300	gat Asp	tta Leu	tta Leu	aca Thr	912
- 1													aaa Lys				960
													aac Asn				1008
													gac Asp				1056
													ccg Pro 365				1104
													gat Asp				1152
1													cat His				1200
													gtt Val				1248
(tgc Cys	aat Asn	tta Leu	ctg Leu 420	agg Arg	ttt Phe	aga Arg	aat Asn	act Thr 425	tct Ser	gaa Glu	gcg Ala	ttt Phe	gat Asp 430	t t g Leu	gaa Glu	1296
1	gga Gly	agt Ser	ata Ile 435	gaa Glu	att	gag Glu	aca Thr	cct Pro 440	agc Ser	tca Ser	aat Asn	gaa Glu	atc lie 445	gtt Val	att	att	1344
,	cgc Arg	aaa Lys 450	aac Asn	aaa Lys	aca Thr	aat Asn	aaa Lys 455	att He	aca Thr	gcg Ala	aca Thr	tta Leu 460	aaa Lys	gca Ala	aat Asn	t ta Leu	1392
:	agt Ser 465	act Thr	aaa Lys	aca Thr	ttc Phe	caa Gin 470	atc ile	agc Ser	gaa Glu	aat Asn	gaa Glu 475	aga Arg	aa t Asn	att Ile	tta Leu	att ile 480	1440
	taa																1443
	(210		20														

Met Gin lie Lys Asn Lys Ala Met Leu lie Thr Tyr Ser Asp Ser Leu 1 10 15

^{\(\}frac{211}{2} \) 20 \(\frac{211}{2} \) 480 \(\frac{212}{2} \) PRT \(\frac{2213}{2} \) Listeria monocytogenes

Gly Lys Asn Met Glu Glu Leu Ser Lys Val Met Glu Thr Tyr Phe Glu 20 25 30 Asp Ala Val Gly Gly IIe His Leu Leu Pro Phe Phe Pro Ser Thr Gly 35 40 45 Asp Arg Gly Phe Ala Pro Ser Asp Tyr Thr Thr Val Asp Ser Asp Leu 50 60 Gly Ser Trp Głu IIe IIe Glu Lys Leu Gly Glu Lys Tyr Tyr Leu Met 65 70 75 80Phe Asp Phe Met Ile Asn His Ile Ser Arg Glu Ser Leu Phe Phe Gln 85 90 95 Asp Phe Lys Lys Glu His Leu Asn Ser Lys Tyr Lys Asp Met Phe Ile 100 105 110 Arg IIe Asn Asp Phe Phe Pro Pro Gly Arg Pro Asn Glu Lys Asp Leu 115 120 125 Asp Leu lie Tyr Lys Arg Lys Asp Lys Ala Pro Phe Gin Glu Val Glu 130 135 140 Phe Ala Asp Gly Gly Thr Glu Leu Val Trp Asn Thr Phe Gly Glu Glu 145 150 155 160 Głn IIe Asp Leu Asp Val Thr Ala Glu Val Thr Lys Glu Phe IIe Arg 165 170 175 Gin Thr ile Lys Asn Met Ala Ala His Gly Cys Ser Ile Leu Arg Leu 180 185 190 Asp Ala Phe Ala Tyr Ala IIe Lys Lys Leu Asp Thr Asn Asp Phe Phe 195 200 205 Val Glu Pro Glu Ile Trp Asp Leu Leu Asp Glu Val Lys Ala Glu Ala 210 215 220 Ala Lys Tyr Asp Met Glu Leu Leu Pro Glu lle His Glu His Tyr Ser 225 230 235 240 lle Gin Met Lys ile Ala Asn His Asp Tyr Tyr lle Tyr Asp Phe Ala 245 250 255 Leu Pro Met Val Met Leu Tyr Ser Leu Tyr Ser Gly Arg Val Glu Arg 260 265 270 Leu Ala Lys Trp Leu Glu Met Ser Pro Met Lys Gln Phe Thr Thr Leu 275 280 285 Asp Thr His Asp Gly IIe Gly Val Val Asp Ala Arg Asp Leu Leu Thr 290 295 300 Asp Glu Glu Leu Asp Tyr Thr Ser Ala Glu Leu Tyr Lys ile Gly Ala 305 310 315 320 Asn Val Lys Lys lie Tyr Ser Ser Glu Lys Tyr Asn Asn Leu Asp lie 325 330 335

Tyr Gin lie Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Lys 340 345

Ser Tyr Leu Leu Ala Arg Val IIe Gin Cys Phe Ala Pro Gly IIe Pro 355 360 365

Gin lie Tyr Tyr Vai Gly Leu Leu Ala Gly Lys Asn Asp lie Asp Leu 370 375 380

Leu Glu Glu Thr Lys Glu Gly Arg Asn IIe Asn Arg His Tyr Tyr Thr 385 390 395 400

ile Asp Glu lle Lys Asn Glu Vai Lys Arg Pro Val Val Lys Ala Leu 405 410 415

Cys Asn Leu Leu Arg Phe Arg Asn Thr Ser Glu Ala Phe Asp Leu Glu 420 425 430

Gly Ser lie Glu lie Glu Thr Pro Ser Ser Asn Giu lie Val lie lie 435 440 445

Arg Lys Asn Lys Thr Asn Lys IIe Thr Ala Thr Leu Lys Ala Asn Leu $450 \hspace{1.5cm} 455 \hspace{1.5cm} 460$

Ser Thr Lys Thr Phe Gin Ile Ser Glu Asn Glu Arg Asn Ile Leu Ile 465 470 475 480

- <210> 21 <211> 1443
- ₹212> DNA
- <213> Artificial Sequence
- <220>
 <223> A mutant of Streptococcus mutans sucrose phyophorylase
- <220> <221> CDS <222> (1)..(1443)
- <400> 21
 atg cca att aca aat aaa aca atg ttg att act tac gca gac agt ttg
 Met Pro lle Thr Asn Lys Thr Met Leu lle Thr Tyr Ala Asp Ser Leu
 1 5 10
 15
- gat gct gtt ggc ggt gtc cat ttg ctg cca ttc ttt cct tcc tca ggt
 Asp Ala Val Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Ser Gly
 35 40 45
- gat cgt ggc ttt gca ccg att gat tac cat gaa gtt gac cct gct ttt
 Asp Arg Gly Phe Ala Pro 11e Asp Tyr His Glu Val Asp Pro Ala Phe
 50 55 60
- ggc gat tgg gat gat gtc aaa cgt ttg ggt gaa aaa cat tac ctc atg Gly Asp Trp Asp Asp Val Lys Arg Leu Gly Glu Lys His Tyr Leu Met 65 70 75 80
- ttt gat ttc atg att aat cat att tcg cgt cag tct aaa tat tat aaa Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys 85 90 95
- gat tac caa gaa aag cat gaa gca agt gct tat aaa gat cta ttt tta Asp Tyr Gln Glu Lys His Glu Ala Ser Ala Tyr Lys Asp Leu Phe Leu
 100 105 110
- aat tgg gat aaa ttt tgg cct aaa aat cgc ccg aca caa gaa gat ctg
 Asn Trp Asp Lys Phe Trp Pro Lys Asn Arg Pro Thr Gin Glu Asp Leu
 115 120 125
- gac ctg att tat aag cgt aag gat cga gca cct atg cag gaa atc cga Asp Leu IIe Tyr Lys Arg Lys Asp Arg Ala Pro Met Gin Giu Iie Arg 130 135 140
- ttt gca gat ggc agt gtt gaa cat ctc tgg agc act ttt ggg gag gaa Phe Ala Asp Gly Ser Val Glu His Leu Trp Ser Thr Phe Gly Glu Glu

EG01	ı 4US-	-Seqi	uenc	e Li:	sting	g. tx	t	Pag	ge 3:	3			
145					150					155			160
		gat Asp											
		att He											

528

576

gat gcc ttt gct tat gct gtt aaa aag cta gat acg aat gat ttc ttt Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe 195 200 205

gtt gaa cct gaa atc tgg act ctg cta gat aaa gtt cgt gat ata gct
Vai Giu Pro Giu lie Trp Thr Leu Leu Asp Lys Vai Arg Asp lie Ala
210 215 220

gct gta tcg ggt gcg gaa atc ttg ccg gaa att cat gaa cac tat act
Ala Val Ser Gly Ala Glu !le Leu Pro Glu !le His Glu His Tyr Thr
225 230 240

att caa ttt aaa att gca gac cat ggt tac tat gtt tat gat ttt gcc 768 lle Gin Phe Lys Ile Ala Asp His Gly Tyr Tyr Val Tyr Asp Phe Ala 245 250 255

ctg cct atg gtg acg ctc tac agc cta tat tcg ggc aag gtt gac cgt
Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Val Asp Arg
260 265 270

ctt gcc aaa tgg ctg aaa atg agt ccg atg aaa cag ttc acc acc ctt
Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gin Phe Thr Thr Leu
275 280 285

gat aca cat gac ggt att ggt gtg gtt gat gtt aag gat atc ctg act
Asp Thr His Asp Gly lle Gly Val Val Asp Val Lys Asp lle Leu Thr
290 295 300

gac gaa gaa att acc tat act tct aat gag ctt tat aag gtc ggt gcc Asp Glu Glu lle Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Ala 305 310 320

aat gtc aat cgt aag tat tca act gcc gaa tat aat aac ttg gat atc
Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp lle
325
330
335

tat caa att aat tca act tac tat tca gca ctt ggt gat gat caa
Tyr Gin ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Gin
340
345

aaa tac ttt ttg gcc cgc ttg ata caa gct ttt gct cca ggt att cca Lys Tyr Phe Leu Ała Arg Leu ile Gin Ala Phe Ala Pro Giy ile Pro 355 360 365

cag gtt tat tac gtt ggc ttt tta gct ggc aag aat gat ctt gaa tta
Gln Vai Tyr Tyr Vai Gly Phe Leu Ala Gly Lys Asn Asp Leu Glu Leu
370 380

ctg gaa agc act aaa gaa ggc cgc aat atc aac cgt cat tat tat agt Leu Giu Ser Thr Lys Giu Giy Arg Asn ile Asn Arg His Tyr Tyr Ser 385 390 395 400

agt gaa gaa att gct aag gaa gtg aag cgg cca gtt gtc aag gca ctt Ser Glu Glu lie Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu 405 410 415

tta aat ctc ttt act tac cgc aat cag tca gca gct ttt gat ttg gat Leu Asn Leu Phe Thr Tyr Arg Asn Gin Ser Ala Ala Phe Asp Leu Asp 420 425 430

ggc cgt att gaa gtg gaa acg cca aat gaa gcg acc att gtc ata gaa Gly Arg lle Glu Val Glu Thr Pro Asn Glu Ala Thr lle Val lle Glu 435 440 445

cgt caa aat aaa gat ggc agt cat atc gca aca gca gag att aat ctc
Arg Gin Asn Lys Asp Gly Ser His Ile Ala Thr Ala Glu Ile Asn Leu
450
460

caa gat atg aca tac aga gta aca gaa aat gat caa aca ata agc ttt Gin Asp Met Thr Tyr Arg Val Thr Giu Asn Asp Gin Thr Iie Ser Phe 465 470 480

Artificial Sequence

<220> <223> Synthetic Construct

<400> 22

Met Pro lie Thr Asn Lys Thr Met Leu lie Thr Tyr Ala Asp Ser Leu 1 5 10 15

Gly Lys Asn Leu Lys Glu Leu Asn Glu Asn Ile Glu Asn Tyr Phe Gly 20 25 30

Asp Ala Val Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Ser Gly 35 40 45

Asp Arg Gly Phe Ala Pro IIe Asp Tyr His Glu Val Asp Pro Ala Phe 50 55 60

Gly Asp Trp Asp Asp Val Lys Arg Leu Gly Glu Lys His Tyr Leu Met 65 70 75 80

Phe Asp Phe Met IIe Asn His IIe Ser Arg Gln Ser Lys Tyr Tyr Lys 85 90 95

Asp Tyr Gln Glu Lys His Glu Ala Ser Ala Tyr Lys Asp Leu Phe Leu 100 105 110

Asn Trp Asp Lys Phe Trp Pro Lys Asn Arg Pro Thr Gin Glu Asp Leu 115 120 125

Asp Leu lie Tyr Lys Arg Lys Asp Arg Ala Pro Met Gin Glu lie Arg 130 135 140

Phe Ala Asp Gly Ser Val Glu His Leu Trp Ser Thr Phe Gly Glu Glu 145 150 155 160

Gin ile Asp Leu Asp Vai Thr Lys Giu Vai Thr Met Asp Phe ile Arg 165 170 175

Ser Thr lie Glu Asn Leu Ala Ala Asn Gly Cys Asp Leu lie Arg Leu 180 185 190

Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe 195 200 205

Val Glu Pro Glu lle Trp Thr Leu Leu Asp Lys Val Arg Asp lle Ala 210 215 220

Ala Val Ser Gly Ala Glu lle Leu Pro Glu lle His Glu His Tyr Thr 225 230 235 240

lle Gin Phe Lys lie Ala Asp His Gly Tyr Tyr Val Tyr Asp Phe Ala 245 250 255

Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Val Asp Arg 260 265 270

Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gin Phe Thr Thr Leu 275 280 285

Asp Thr His Asp Gly Ile Gly Val Val Asp Val Lys Asp Ile Leu Thr

```
EG014US-Sequence Listing.txt
                                      Page 35
Asp Glu Glu lle Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Ala
305 310 315 320
Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp Ile
325 330 335
Tyr Gin ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Gin 340 345
Lys Tyr Phe Leu Ala Arg Leu IIe Gin Ala Phe Ala Pro Giy IIe Pro 355 360 365
Gin Vai Tyr Tyr Vai Gly Phe Leu Ala Gly Lys Asn Asp Leu Glu Leu
370 375 380
Leu Giu Ser Thr Lys Giu Giy Arg Asn IIe Asn Arg His Tyr Tyr Ser
385 390 395 400
Ser Glu Glu IIe Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu
405 410 415
Leu Asn Leu Phe Thr Tyr Arg Asn Gin Ser Ala Ala Phe Asp Leu Asp 420 425 430
Gly Arg lie Glu Val Glu Thr Pro Asn Glu Ala Thr lie Val ile Glu 435 440 445
Arg Gin Asn Lys Asp Gly Ser His lie Ala Thr Ala Glu lle Asn Leu 450 455 460
Gin Asp Met Thr Tyr Arg Val Thr Giu Asn Asp Gin Thr Ile Ser Phe
465 470 475 480
Glu
       Artificial Sequence
<220>
<221> CDS
<222> (1)..(1461)
atg cca att aca aat aaa aca atg ttg att act tac gca gac agt ttg
Met Pro lie Thr Asn Lys Thr Met Leu lie Thr Tyr Ala Asp Ser Leu
1 5 10 15
96
gat gct gtt ggc ggt gtc cat ttg ctg cca ttc ttt cct tcc aca ggt
Asp Ala Val Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
35 40 45
                                                                                144
```

gat cgt ggc ttt gca ccg att gat tac cat gaa gtt gac tct gct ttt Asp Arg Gly Phe Ala Pro lle Asp Tyr His Glu Val Asp Ser Ala Phe 50 55 60

ggc gat tgg gat gat gtc aaa cgt ttg ggt gaa aaa tat tac ctc atg Gly Asp Trp Asp Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met 65 70 75 80 240

											•					
EG0	14US	-Seq	uenc	e Li	stin	g. tx	t	Pa	ge 3	6						
ttt Phe	gat Asp	ttc Phe	atg Met	att Ile 85	aa t As n	cat His	att	tcg Ser	cgt Arg 90	cag Gin	tct Ser	aaa Lys	tat Tyr	tat Tyr 95	aaa Lys	288
				Lys										Phe	tta Leu	336
			Lys					Asn			aca Thr					384
											aag Lys 140					432
											act Thr					480
cag Gin	att	gat Asp	ctt Leu	gac Asp 165	gtg Val	act Thr	aaa Lys	gaa Glu	gtg Val 170	act Thr	atg Met	gat Asp	ttt Phe	att Ile 175	Arg	528
											gat Asp					576
											acg Thr					624
gtt Val	gaa Glu 210	cct Pro	gaa Glu	atc He	tgg Trp	act Thr 215	ctg Leu	cta Leu	gat Asp	aaa Lys	gtt Val 220	cgt Arg	gat Asp	ata Ile	gc t Ala	672
											cat His					720
											gtt Val					768
											ggc Gly					816
											cag Gin					864
gat Asp	aca Thr 290	cat His	gac Asp	ggt Gly	att	ggt Gly 295	gtg Val	gtt Val	gat Asp	gtt Val	aag Lys 300	gat Asp	atc lle	ctg Leu	act Thr	912
											tat Tyr					960
											aa t As n					1008
tat Tyr	caa Gin	att	aat Asn 340	tca Ser	ac t Thr	tac Tyr	tat Tyr	tca Ser 345	gca Ala	ctt Leu	gg t Gly	gat Asp	gat Asp 350	gat Asp	caa GIn	1056
											gc t Ala					1104
											aat Asn 380					1152
											cgt Arg					1200
agt Ser	gaa Glu	gaa Glu	att ile	gct Ala 405	aag Lys	gaa Glu	gtg Val	aag Lys	cgg Arg 410	cca Pro	gtt Val	gtc Val	aag Lys	gca Ala 415	ctt Leu	1248
tta	aat	ctc	ttt	act	tac	cgc	aat	cag	tca	gca	gct	ttt	gat	ttg	gat	1296

EG014US-Sequence Listing.txt Page 37													
Leu Asn I	Leu Ph		Tyr	Arg	Asn	Gin 425	Ser	Ala	Ala	Phe	Asp 430		Asp
ggc cgt a Gly Arg													
cgt caa Arg Gln 450	aat aa Asn Ly	a gat s Asp	ggc Gly	agt Ser 455	cat His	atc	gca Ala	aca Thr	gca Ala 460	gag Glu	att	aat Asn	ctc Leu
caa gat a GIn Asp ! 465	atg ac Met Th	a tac r Tyr	aga Arg 470	gta Vai	aca Thr	gaa Glu	aat Asn	gat Asp 475	caa Gln	aca Thr	ata Ile	agc Ser	tta Leu 480
tcc atg a Ser Met													
<212> PI	4 87 RT rtific	ial Se	equer	ıce									
<220> <223> Sy	ynthet	i c Cor	nstru	ıct									
<400> 24	4												
Met Pro 1	lle Th	r Asn 5	Lys	Thr	Met	Leu	e 10	Thr	Tyr	Ala	Asp	Ser 15	Leu
Gly Lys /	Asn Lei 20	ı Lys	Glu	Leu	Asn	G1 u 25	Аѕл	He	Glu	Asn	Tyr 30	Phe	Gly
Asp Ala \	Val Gly 35	Gly	Val	His	Leu 40	Leu	Pro	Phe	Phe	Pro 45	Ser	Thr	Gly
Asp Arg (Gly Phe	. Ala	Pro	11e 55	Asp	Tyr	His	Glu	Va I 60	Asp	Ser	Ala	Phe
Gly Asp 7 65	Trp Ast	Asp	Va I 70	Lys	Arg	Leu	Gly	G I u 75	Lys	Tyr	Tyr	Leu	Met 80
Phe Asp F	he Mei	11e 85	Asn	His	lie	Ser	Arg 90	GIn	Ser	Lys	Tyr	Tyr 95	Lys
Asp Tyr (Gin Gir 100		His	Glu	Ala	Ser 105	Ala	Tyr	Lys	Asp	Leu 110	Phe	Leu
Asn Trp A	Asp Lys 115	Phe	Trp	Pro	Lys 120	Asn	Arg	Pro	Thr	GI n 125	Glu	Asp	Val
Asp Leu 1 130	lle Tyr	Lys	Arg	Lys 135	Asp	Arg	Ala	Pro	Lys 140	Gln	Glu	lle	GIn
Phe Ala A 145	Asp Gly	Ser	Va I 150	Glu	His	Leu	Trp	Asn 155	Thr	Phe	Gly	Glu	G I u 160
Gin lie A	Asp Leu	Asp 165	Val	Thr	Lys	Glu	Val 170	Thr	Met	Asp	Phe	lle 175	Arg
Ser Thr I	lle Glu 180		Leu	Ala	Ala	Asn 185	Gly	Cys	Asp	Leu	lle 190	Arg	Leu
Asp Ala P	Phe Ala 195	Tyr	Ala		Lys 200	Lys	Leu	Asp.		Asn 205	Asp	Phe	Phe
Val Glu P 210	Pro Glu	He		Thr 215	Leu	Leu	Asp		Val 220	Arg	Asp	lle	Ala

EG014US-Sequence Listing.txt Page 38

Ala Val Ser Gly Ala Glu IIe Leu Pro Glu IIe His Glu His Tyr Thr 225 230 235 240

lle Gln Phe Lys lle Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala 245 250 255

Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Val Asp Arg 260 270

Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gin Phe Thr Thr Leu 275 280 285

Asp Thr His Asp Gly IIe Gly Val Val Asp Val Lys Asp IIe Leu Thr 290 295 300

Asp Glu Glu lie Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Vai Gly Ala 305 310 315

Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp lle 325 330 335

Tyr Gin lie Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Gin 340 350

Lys Tyr Phe Leu Ala Arg Leu IIe Gin Ala Phe Ala Pro Gly IIe Pro 355 360 365

Gin Vai Tyr Tyr Vai Giy Phe Leu Ala Giy Lys Asn Asp Leu Giu Leu 370 375 380

Leu Glu Ser Thr Lys Glu Gly Arg Asn IIe Asn Arg His Tyr Tyr Ser 385 390 395 400

Ser Glu Glu IIe Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu 405 410 415

Leu Asn Leu Phe Thr Tyr Arg Asn Gin Ser Ala Ala Phe Asp Leu Asp 420 430

Gly Arg lle Glu Val Glu Thr Pro Asn Glu Ala Thr lle Val lle Glu 435 440 445

Arg Gin Asn Lys Asp Gly Ser His lie Ala Thr Ala Glu ile Asn Leu 450 460

Gin Asp Met Thr Tyr Arg Val Thr Giu Asn Asp Gin Thr lie Ser Leu 465 470 475 480

Ser Met Ile Ser Cys Gln Thr 485

<210> 25 <211> 56 <212> PRT <213> Streptococcus mutans

Ala Val Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly Asp 1 10 15

Arg Gly Phe Ala Pro IIe Asp Tyr His Glu Val Asp Ser Ala Phe Gly 20 25 30

Asp Trp Asp Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met Phe

```
EGO14US-Sequence Listing.txt Page 39

35 40 45

Asp Phe Met IIe Asn His IIe Ser
50 55

C210> 26
C211> 42
C212> PRT
C213> Streptococcus mutans
C400> 26

Arg Pro Thr Gin Giu Asp Val Asp Leu IIe Tyr Lys Arg Lys Asp Arg
1 5

Ala Pro Lys Gin Giu IIe Gin Phe Ala Asp Giy Ser Val Giu His Leu
20 25

Trp Asn Thr Phe Giy Giu Giu Gin IIe Asp
40 10

C210> 27
C211> 38
C212> PRT
C213> Streptococcus mutans
C400> 27
IIe Leu Pro Giu IIe His Giu His Tyr Thr IIe Gin Phe Lys IIe Ala
1 5

Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala Leu Pro Met Val Thr Leu
20 25

Tyr Ser Leu Tyr Ser Giy
```